

\$%^STN;HighlightOn= ***;HighlightOff=*** ;

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NEWS	1		Web Page URLs for STN Seminar Schedule - N. America
NEWS	2		"Ask CAS" for self-help around the clock
NEWS	3	SEP 09	CA/CAPLUS records now contain indexing from 1907 to the present
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NEWS	7	OCT 21	BIOSIS file reloaded and enhanced
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NEWS	9	NOV 24	MSDS-CCOHS file reloaded
NEWS	10	DEC 08	CABA reloaded with left truncation
NEWS	11	DEC 08	IMS file names changed
NEWS	12	DEC 09	Experimental property data collected by CAS now available in REGISTRY
NEWS	13	DEC 09	STN Entry Date available for display in REGISTRY and CA/CAPLUS
NEWS	14	DEC 17	DGENE: Two new display fields added
NEWS	15	DEC 18	BIOTECHNO no longer updated
NEWS	16	DEC 19	CROPU no longer updated; subscriber discount no longer available
NEWS	17	DEC 22	Additional INPI reactions and pre-1907 documents added to CAS databases
NEWS	18	DEC 22	IFIPAT/IFIUDB/IFICDB reloaded with new data and search fields
NEWS	19	DEC 22	ABI-INFORM now available on STN
NEWS	20	JAN 27	Source of Registration (SR) information in REGISTRY updated and searchable
NEWS	21	JAN 27	A new search aid, the Company Name Thesaurus, available in CA/CAPLUS
NEWS	22	FEB 05	German (DE) application and patent publication number format changes

NEWS EXPRESS	DECEMBER 28 CURRENT WINDOWS VERSION IS V7.00, CURRENT MACINTOSH VERSION IS V6.0b(ENG) AND V6.0Jb(JP), AND CURRENT DISCOVER FILE IS DATED 23 SEPTEMBER 2003
NEWS HOURS	STN Operating Hours Plus Help Desk Availability
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* * * * * STN Columbus * * * * *

FILE 'HOME' ENTERED AT 10:42:23 ON 01 MAR 2004

=> index biosci

FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED

COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
0.21	0.21

FULL ESTIMATED COST

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, AQUASCI, BIOBUSINESS, BIOCOMMERCE, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CANCERLIT, CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI, CROPB, CROPU, DISSABS, DDFB, DDFU, DGENE, DRUGB, DRUGMONOG2, ...' ENTERED AT 10:42:36 ON 01 MAR 2004

68 FILES IN THE FILE LIST IN STNINDEX

Enter SET DETAIL ON to see search term postings or to view search error messages that display as 0* with SET DETAIL OFF.

=> s (transfection (w) agent) (P) (peptide or polypeptide)

- 0* FILE ADISNEWS
- 0* FILE BIOCOMMERCE
- 10 FILE BIOSIS
- 16* FILE BIOTECHABS
- 16* FILE BIOTECHDS
- 4* FILE BIOTECHNO
- 3 FILE CANCERLIT
- 9 FILE CAPLUS
- 2* FILE CEABA-VTB
- 1* FILE CIN
- 1 FILE DISSABS
- 2 FILE DDFU
- 77 FILE DGENE

25 FILES SEARCHED...

- 2 FILE DRUGU
- 3 FILE EMBASE
- 4* FILE ESBIODBASE
- 1* FILE FEDRIP
- 0* FILE FOMAD
- 0* FILE FOREGE
- 0* FILE FROSTI
- 0* FILE FSTA
- 14 FILE IFIPAT
- 0* FILE KOSMET
- 2 FILE LIFESCI
- 0* FILE MEDICONF
- 4 FILE MEDLINE
- 0* FILE NTIS

0* FILE NUTRACEUT
0* FILE PHARMAML
57 FILES SEARCHED...
4 FILE SCISEARCH
5 FILE TOXCENTER
21 FILE USPATFULL
14 FILE WPIDS
14 FILE WPINDEX

23 FILES HAVE ONE OR MORE ANSWERS, 68 FILES SEARCHED IN STNINDEX

L1 QUE (TRANSFECTION (W) AGENT) (P) (PEPTIDE OR POLYPEPTIDE)

=> file hits

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	1.71	1.92

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=> s l1

PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'AGENT) (P) '
5 FILES SEARCHED...

PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'AGENT) (P) '
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'AGENT) (P) '
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'AGENT) (P) '
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'AGENT) (P) '
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'AGENT) (P) '
L2 197 L1

=> s (hydrophobic (w) domain) and aromatic
L3 2082 (HYDROPHOBIC (W) DOMAIN) AND AROMATIC

=> s (hydrophilic (w) domain) and basic
L4 327 (HYDROPHILIC (W) DOMAIN) AND BASIC

=> s l2 and l3 and l4
L5 1 L2 AND L3 AND L4

=> d l5 bib ab

L5 ANSWER 1 OF 1 USPATFULL on STN

AN 2003:173877 USPATFULL
 TI Peptide-mediated transfection agents and methods of use
 IN Divita, Gilles, Paris, FRANCE
 Morris, May C., Paris, FRANCE
 Mery, Jean, Paris, FRANCE
 Heitz, Frederic, Paris, FRANCE
 Fernandez, Joseph, Carlsbad, CA, UNITED STATES
 Archdeacon, John, Carlsbad, CA, UNITED STATES
 Hondorp, Kyle, Carlsbad, CA, UNITED STATES
 PI US 2003119725 A1 20030626
 AI US 2001-915914 A1 20010726 (9)
 PRAI US 2000-221932P 20000731 (60)
 DT Utility
 FS APPLICATION
 LREP DAVID R PRESTON & ASSOCIATES, 12625 HIGH BLUFF DRIVE, SUITE 205, SAN
 DIEGO, CA, 92130
 CLMN Number of Claims: 75
 ECL Exemplary Claim: 1
 DRWN 26 Drawing Page(s)
 LN.CNT 4044
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.
 AB Peptides that are useful as transfection agents are described. The
 peptides can facilitate the efficient cellular internalization of a
 broad range and size of compounds that when non-covalently complexed
 therewith are efficiently internalized into a cell. Advantages include
 but are not limited to excellent transfection efficiency, relatively low
 toxicity, internalization by a broad host cell spectrum, and the
 simplicity and cost-effectiveness that arise from not having to
 covalently complex the peptide with a specific molecule to be delivered.
 Applications include but are not limited to the delivery of diagnostics
 and therapeutics, as well as drug discovery, gene discovery, and the
 analysis and/or manipulation of other cellular and molecular biological
 functions. claims are made for transfection agents, compositions of
 matter, including pharmaceutical compositions, reagent kits, methods of
 delivery, and methods of identification of additional peptides for
 performing and/or including in the same.

=> log h

COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	59.45	61.37

SESSION WILL BE HELD FOR 60 MINUTES
 STN INTERNATIONAL SESSION SUSPENDED AT 10:46:33 ON 01 MAR 2004

OM protein - protein search, using sw model

Run on: March 1, 2004, 13:31:13 ; Search time 53.0189 Seconds
(without alignments)
106.584 Million cell updates/sec

Title: US-09-915-914B-8
Perfect score: 130
Sequence: 1 KETWETWTEWSQPKRKV 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			ID	Description
	Score	Match	Length		
1	130	100.0	20	5 ABB77672	Abb77672 Peptide t
2	120	92.3	21	5 ABG78995	Abg78995 Cell pene
3	120	92.3	21	5 ABB77693	Abb77693 Peptide t
4	120	92.3	21	5 ABB77671	Abb77671 Peptide t
5	120	92.3	21	7 ADB68484	Adb68484 Peptide s
6	120	92.3	21	7 ADC22460	Adc22460 Protein-d
7	116	89.2	20	5 ABB77673	Abb77673 Peptide t
8	110	84.6	20	5 ABB77694	Abb77694 Peptide t
9	109	83.8	19	5 ABB10106	Abb10106 Peptide t

10	108	83.1	21	5 ABB77674	Abb77674 Peptide t
11	95	73.1	19	5 ABB77699	Abb77699 Peptide t
12	93	71.5	19	5 ABB77676	Abb77676 Peptide t
13	90	69.2	12	5 ABB77689	Abb77689 Hydrophob
14	90	69.2	12	5 ABP56174	Abp56174 Cell-targ
15	90	69.2	26	5 ABP56200	Abp56200 Chimeric
16	87	66.9	19	5 ABB77675	Abb77675 Peptide t
17	82	63.1	21	5 ABB77678	Abb77678 Generic p
18	79	60.8	11	5 ABB77695	Abb77695 Peptide t
19	73	56.2	17	5 ABB77667	Abb77667 Peptide t
20	69	53.1	9	5 ABB77692	Abb77692 Peptide t
21	69	53.1	18	5 ABB77666	Abb77666 Peptide t
22	69	53.1	19	5 ABB77668	Abb77668 Peptide t
23	69	53.1	19	5 ABB77698	Abb77698 Peptide t
24	69	53.1	19	5 ABB77669	Abb77669 Peptide t
25	69	53.1	20	5 ABB77679	Abb77679 Generic p
26	64	49.2	19	5 ABB77670	Abb77670 Peptide t
27	61.5	47.3	430	5 ABP47755	Abp47755 Protein #
28	61.5	47.3	560	4 AAB84201	Aab84201 Amino aci
29	61.5	47.3	560	6 AAG79973	Ag79973 P2C/C38S/
30	61.5	47.3	560	7 ADE29023	Ade29023 HIV-1 RT
31	61.5	47.3	562	6 ABR44741	Abr44741 Plasmid p
32	61.5	47.3	562	6 ABR44740	Abr44740 Plasmid p
33	61.5	47.3	565	6 ABR44743	Abr44743 Plasmid 7
34	61.5	47.3	724	5 AAU11869	Aaul1869 HIV pol p
35	61.5	47.3	739	5 AAU11874	Aaul1874 HIV pol p
36	61.5	47.3	760	1 AAP94510	Aap94510 Sequence
37	61.5	47.3	850	4 AAE04792	Aae04792 Human imm
38	61.5	47.3	850	4 AAE04791	Aae04791 Human imm
39	61.5	47.3	850	5 ADE71141	Ade71141 Codon opt
40	61.5	47.3	850	5 ADE71143	Ade71143 Inactivat
41	61.5	47.3	850	6 ABU63365	Abu63365 HIV-1 wil
42	61.5	47.3	850	6 ABU63366	Abu63366 HIV-1 ina
43	61.5	47.3	875	4 AAE04794	Aae04794 Human tPA
44	61.5	47.3	875	4 AAE04793	Aae04793 Human tPA
45	61.5	47.3	875	5 ADE71145	Ade71145 Codon opt

ALIGNMENTS

RESULT 1
ABB77672
ID ABB77672 standard; peptide; 20 AA.
XX
AC ABB77672;
XX
DT 01-JUL-2002 (first entry)
XX
DE Peptide transfection agent Pep-2.1.
XX
KW Intracellular delivery; transfection agent; cancer; infectious disease;
KW peptide vector.
XX
OS Synthetic.
XX
PN WO200210201-A2.

XX 07-FEB-2002.
XX PD
XX PF 26-JUL-2001; 2001WO-US023406.
XX PR 31-JUL-2000; 2000US-0221932P.
XX PA (ACTI-) ACTIVE MOTIF.
XX PA (CNRS) CENT NAT RECH SCI.
XX PI Divida G, Morris M, Mery J, Heitz F, Fernandez J, Archdeacon J;
PI Horndorp K;
XX WPI; 2002-329441/36.
XX
PT Transfection agent that comprises a peptide comprising hydrophobic and
PT hydrophilic domain and having amino acid residues of specified length is
PT useful for a non-covalent association with and transport of a
PT heterologous compound into a cell.
XX
XX Claim 12; Page 17; 156pp; English.
XX
CC The invention relates to a transfection agent comprises a peptide of
CC about 16 - 30 amino acids in length. Peptides of the invention comprise a
CC hydrophobic domain, a hydrophilic domain, optionally a spacer sequence
CC between the domains and a functional group conjugated to at least one
CC terminal of the peptide. Peptides of the invention are useful for a non-
CC covalent association with and transport of a heterologous compound into a
CC cell. They are also useful for promoting the cellular internalisation of
CC at least one member e.g. peptide, proteins, antibodies, their derivatives
CC and/or conjugates. They may form part of a pharmaceutical composition to
CC deliver the compound selected from a diagnostic or therapeutic compound,
CC to treat at least one condition such as cancer or an infectious disease,
CC or which targets a cancerous cell or pathogen-infected cell and to
CC deliver a peptide or inhibitor that disrupts the activity of the enzyme.
CC The agent of the invention has a transfection efficiency of at least 5%
CC for at least two of the members of the group of the compounds. The agent
CC has a good delivery efficiency for a broad spectrum of compounds and cell
CC types, has a low toxicity, are easy to handle and easy to formulate in
CC conjunction with the many different compound types that it can deliver.
CC The peptides are serum sensitive, thus they bode particularly well for
CC systemic and/or localised in patients. The current sequence represents
CC the peptide transfection agent Pep-2.1
XX
SQ Sequence 20 AA;
Query Match 100.0%; Score 130; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.3e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KETWETWWTWSQPKRKV 20
Db 1 KETWETWWTWSQPKRKV 20
Search completed: March 1, 2004, 16:55:55
Job time : 53.0189 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: March 1, 2004, 16:46:26 ; Search time 13.1132 Seconds
(without alignments)
146.709 Million cell updates/sec

Title: US-09-915-914B-8
Perfect score: 130
Sequence: 1 KETWETWWTWSQPKRKV 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match %	Length DB ID	Description
1	61.5	47.3	559 2	B47175 reverse transcript
2	61.5	47.3	1003 1	GNVWL HIV-1 retropepsin
3	61.5	47.3	1003 1	B44001 HIV-1 retropepsin
4	61.5	47.3	1003 2	T09440 pol polyprotein -
5	61.5	47.3	1012 1	GNVWL HIV-1 retropepsin
6	61.5	47.3	1015 1	GNVWH3 HIV-1 retropepsin
7	56.5	43.5	902 2	T01668 pol polyprotein -
8	56.5	43.5	1002 2	S54378 pol polyprotein -
9	56.5	43.5	1451 2	B86286 F911.15 protein -
10	56.5	43.5	1469 2	H96622 probable ABC trans
11	55.5	42.7	1002 1	GNLJND HIV-1 retropepsin
12	53	40.8	374 2	AG0937 hypothetical prote
13	53	40.8	689 2	F83902 beta-galactosidase

14 hypothetical prote
15 hypothetical prote
16 hypothetical 48K p
17 reverse transcript
18 pol polypeptin -
19 HIV-1 retropepsin
20 hypothetical prote
21 hypothetical prote
22 beta-galactosidase
23 conserved hypothet
24 ecdysone-inducible
25 cytochrome P450-li
26 chitinase VCA0027
27 ecdysone-inducible
28 SYG1 protein - yea
29 poly(3-hydroxyalka
30 hypothetical prote
31 hypothetical prote
32 hypothetical prote
33 probable membrane
34 interleukin-9 rece
35 large T antigen -
36 UV-endonuclease -
37 pol polypeptin -
38 HIV-1 retropepsin
39 HIV-1 retropepsin
40 hypothetical prote
41 hypothetical prote
42 glycine betaine tr
43 glycogen phosphory
44 HIV-1 retropepsin
45 hypothetical prote

52 40.0 413 2 C91229
52 40.0 413 2 B86076
52 40.0 418 2 S40824
50.5 38.8 559 2 A47175
50.5 38.8 912 2 S33980
50.5 38.8 1003 1 GNVWAZ
50 38.5 368 2 T15492
50 38.5 581 2 T38501
50 38.5 686 2 AH0104
50 38.5 818 2 F87327
49 37.7 390 1 B49070
49 37.7 455 2 T48973
49 37.7 849 2 D82310
49 37.7 864 2 A49070
49 37.7 902 2 S49931
48.5 37.3 562 2 S25725
48.5 37.3 770 2 S75042
48.5 37.3 894 2 T27007
48 36.9 45 2 C82233
48 36.9 197 2 S59397
48 36.9 468 2 A45268
48 36.9 586 1 TVVFBP
48 36.9 656 2 S55262
48 36.9 1019 2 T11560
48 36.9 1054 1 GNLJG5
48 36.9 1056 1 GNLJG3
47.5 36.5 239 2 C84505
41 47.5 36.5 315 2 S76267
42 47.5 36.5 544 2 B84264
43 47.5 36.5 692 2 H70362
44 47.5 36.5 1027 1 GNLJSI
47 36.2 463 2 T48116

Search completed: March 1, 2004, 19:34:31
Job time : 14.2041 secs

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CM protein - protein search, using sw model

Run on: March 1, 2004, 16:39:39 ; Search time 8.11321 Seconds
(without alignments)
128.359 Million cell updates/sec

Title: US-09-915-914B-8
Perfect score: 130
Sequence: 1 KETWETWTEWSQPKRKV 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	61.5	47.3	1003	1	POL_HV1H2	P04585 human immun
2	61.5	47.3	1003	1	POL_HV1Y2	P35963 human immun
3	61.5	47.3	1007	1	POL_HV1JR	P20875 human immun
4	61.5	47.3	1015	1	POL_HV1B1	P03366 human immun
5	61.5	47.3	1015	1	POL_HV1B5	P04587 human immun
6	61.5	47.3	1015	1	POL_HV1BR	P03367 human immun
7	61.5	47.3	1015	1	POL_HV1PV	P03368 human immun
8	60.5	46.5	1006	1	POL_HV1MN	P05961 human immun
9	56.5	43.5	1002	1	POL_HV1EL	P04589 human immun
10	56.5	43.5	1002	1	POL_HV1MA	P04588 human immun
11	56.5	43.5	1002	1	POL_HV1RH	P05959 human immun
12	56.5	43.5	1002	1	POL_HV1Z2	P12499 human immun
13	56.5	43.5	1003	1	POL_HV1N5	P12497 human immun
14	56.5	43.5	1003	1	POL_HV1OY	P20892 human immun
15	55.5	42.7	1002	1	POL_HV1ND	P18802 human immun
16	52	40.0	413	1	YIHS_ECOLI	P32140 escherichia
17	50.5	38.8	1002	1	POL_HV1U4	P24740 human immun

18	50.5	38.8	1003	1	POL_HV1A2	P03369	human immun
19	49	37.7	229	1	UNG_CHLCV	Q821f7	chlamyidophi
20	49	37.7	902	1	SYGI_YEAST	P40528	saccharomyc
21	48	36.9	41	1	LPW_VIBPA	P22100	vibrio para
22	48	36.9	468	1	IL9F_MOUSE	Q01114	mus musculu
23	48	36.9	586	1	TALA_POVBO	P24851	bovine poly
24	48	36.9	656	1	UVEI_NEUCR	Q01408	neurospora
25	48	36.9	880	1	SYL_XANAC	Q8piw4	xanthomonas
26	48	36.9	1019	1	POL_SIVS4	P12502	simian immu
27	48	36.9	1022	1	POL_SIVSP	P19505	simian immu
28	48	36.9	1054	1	POL_SIVMK	P05897	simian immu
29	48	36.9	1056	1	POL_SIVM1	P05896	simian immu
30	48	36.9	2298	1	YCF2_LOTJA	Q9b1k6	lotus japon
31	47.5	36.5	315	1	SECF_SYNY3	Q55611	synechocyst
32	47.5	36.5	692	1	PHSG_AQUAE	O66932	aquifex aeo
33	47.5	36.5	1027	1	POL_SIVCZ	P17283	chimpanzee
34	47	36.2	964	1	RRPO_MCMV	P11640	maize chlor
35	46.5	35.8	794	1	YE14_YEAST	P39961	saccharomyc
36	46.5	35.8	1058	1	POL_HV2D2	P15833	human immun
37	46	35.4	78	1	YO09_BPL2	P42544	bacterioph
38	46	35.4	392	1	OR9A_DROME	Q9w2u9	drosophila
39	46	35.4	504	1	MATK_NEPAL	Q95gt2	nepenthes a
40	46	35.4	506	1	MATK_CALVU	O47143	calluna vul
41	46	35.4	513	1	MATK_CYRRA	Q8wiv4	cynilla rac
42	46	35.4	567	1	EIL3_ARATH	O23116	arabidopsis
43	46	35.4	635	1	DAL4_YEAST	Q04895	saccharomyc
44	45.5	35.0	688	1	TALA_POVJC	P03072	polyomaviru
45	45.5	35.0	860	1	LOXA_LYCES	P38415	lycopersico

Search completed: March 1, 2004, 19:25:04
Job time : 10.1132 secs

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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:40:39 ; Search time 37.4528 Seconds
(without alignments)
168.488 Million cell updates/sec

Title: US-09-915-914B-8
Perfect score: 130
Sequence: 1 KETWETWWTWSQPKRKV 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

8			
Result	Query		
No.	Score	Match Length	ID Description

1 64.5 49.6 433 15 Q79787 human immun
2 63 48.5 793 17 Q8TVU1 methanopyru
3 61.5 47.3 212 15 Q9WGU7 human immun
4 61.5 47.3 225 15 Q998V3 human immun
5 61.5 47.3 236 15 Q9WGX3 human immun
6 61.5 47.3 237 15 Q9WGV0 human immun
7 61.5 47.3 237 15 Q9WGV3 human immun
8 61.5 47.3 237 15 Q9WGV7 human immun
9 61.5 47.3 237 15 Q9WGW5 human immun
10 61.5 47.3 237 15 Q9WGW0 human immun
11 61.5 47.3 237 15 Q9WGV5 human immun
12 61.5 47.3 237 15 Q9WGV9 human immun
13 61.5 47.3 237 15 Q9WGH5 human immun
14 61.5 47.3 237 15 Q9W9U0 human immun
15 61.5 47.3 237 15 Q9WGX6 human immun
16 61.5 47.3 237 15 Q9WGW2 human immun
17 61.5 47.3 237 15 Q9WGX5 human immun
18 61.5 47.3 237 15 Q9WGW1 human immun
19 61.5 47.3 237 15 Q9WGV2 human immun
20 61.5 47.3 237 15 Q9WGU8 human immun
21 61.5 47.3 237 15 Q9WGW6 human immun
22 61.5 47.3 237 15 Q9WGV6 human immun
23 61.5 47.3 237 15 Q9WGV8 human immun
24 61.5 47.3 237 15 Q9WGW3 human immun
25 61.5 47.3 237 15 Q9WGW4 human immun
26 61.5 47.3 237 15 Q9WGV1 human immun
27 61.5 47.3 237 15 Q9WGV4 human immun
28 61.5 47.3 514 15 Q9DLJ8 human immun
29 61.5 47.3 519 15 Q9IDI3 human immun
30 61.5 47.3 523 15 Q9IDI9 human immun
31 61.5 47.3 523 15 Q9IDC7 human immun
32 61.5 47.3 523 15 Q9IDB6 human immun
33 61.5 47.3 523 15 Q9IDB2 human immun
34 61.5 47.3 523 15 Q9IDF2 human immun
35 61.5 47.3 523 15 Q9IDB0 human immun
36 61.5 47.3 524 15 Q9IDJ7 human immun
37 61.5 47.3 524 15 Q9IDI8 human immun
38 61.5 47.3 524 15 Q9IDI7 human immun
39 61.5 47.3 524 15 Q9IDD1 human immun
40 61.5 47.3 524 15 Q9IDI6 human immun
41 61.5 47.3 524 15 Q9IDB8 human immun
42 61.5 47.3 524 15 Q9IDI2 human immun
43 61.5 47.3 524 15 Q9IDI4 human immun
44 61.5 47.3 524 15 Q9IDI5 human immun
45 61.5 47.3 524 15 Q9IDD2 human immun

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
OM protein - protein search, using sw model
Run on: March 1, 2004, 13:31:13 ; Search time 53.0189 Seconds
(without alignments)
106.584 Million cell updates/sec

Title: US-09-915-914B-9
Perfect score: 123
Sequence: 1 KETWETWTEASQPKRKV 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	123	100.0	20	5	ABB77673
2	116	94.3	20	5	ABB77672
3	106	86.2	21	5	ABG78995
4	106	86.2	21	5	ABB77693
5	106	86.2	21	5	ABB77671
6	106	86.2	21	7	ADB68484
7	106	86.2	21	7	ADC22460
8	102	82.9	19	5	ABB77699
9	96	78.0	20	5	ABB77694

Search completed: March 1, 2004, 19:31:58
Job time : 37.4528 secs

10 95 77.2 19 5 ABB10106 Abb10106 Peptide t
11 94 76.4 21 5 ABB77674 Abb77674 Peptide t
12 84 68.3 21 5 ABB77678 Abb77678 Generic p
13 79 64.2 11 5 ABB77695 Abb77695 Peptide t
14 79 64.2 12 5 ABB77689 Abb77689 Hydrophob
15 79 64.2 12 5 ABP56174 Abp56174 Cell-targ
16 79 64.2 19 5 ABB77676 Abb77676 Peptide t
17 79 64.2 26 5 ABP56200 Abp56200 Chimeric
18 77 62.6 19 5 ABB77675 Abb77675 Peptide t
19 73 59.3 17 5 ABB77667 Abb77667 Peptide t
20 69 56.1 9 5 ABB77692 Abb77692 Peptide t
21 69 56.1 18 5 ABB77666 Abb77666 Peptide t
22 69 56.1 19 5 ABB77668 Abb77668 Peptide t
23 69 56.1 19 5 ABB77698 Abb77698 Peptide t
24 69 56.1 19 5 ABB77669 Abb77669 Peptide t
25 69 56.1 20 5 ABB77679 Abb77679 Generic p
26 64 52.0 19 5 ABB77670 Abb77670 Peptide t
27 57.5 46.7 10 5 ABB78711 Abb78711 HIV-1 BH1
28 57.5 46.7 21 5 ABB78716 Abb78716 Peptide p
29 57.5 46.7 21 5 ABB77665 Abb77665 Peptide t
30 57.5 46.7 25 5 ABB78714 Abb78714 Retroinhi
31 57.5 46.7 430 5 ABP47755 Abp47755 Protein #
32 57.5 46.7 560 4 AAB84201 Aab84201 Amino aci
33 57.5 46.7 560 6 AAG79973 Aag79973 P2C/C38S/
34 57.5 46.7 560 7 ADE29023 Ade29023 HIV-1 RT
35 57.5 46.7 562 6 ABR44741 Abr44741 Plasmid p
36 57.5 46.7 562 6 ABR44740 Abr44740 Plasmid p
37 57.5 46.7 565 6 ABR44743 Abr44743 Plasmid 7
38 57.5 46.7 724 5 AAU11869 Aau11869 HIV pol p
39 57.5 46.7 739 5 AAU11874 Aau11874 HIV pol p
40 57.5 46.7 760 1 AAP94510 Aap94510 Sequence
41 57.5 46.7 850 4 AAE04792 Aae04792 Human imm
42 57.5 46.7 850 4 AAE04791 Aae04791 Human imm
43 57.5 46.7 850 5 ADE71141 Ade71141 Codon opt
44 57.5 46.7 850 5 ADE71143 Ade71143 Inactivat
45 57.5 46.7 850 6 ABU63365 Abu63365 HIV-1 wil

ALIGNMENTS

RESULT 1
ABB77673
ID ABB77673 standard; peptide; 20 AA.

XX ABB77673;
AC
XX
DT 01-JUL-2002 (first entry)
XX
DE Peptide transfection agent Pep-2.2.
XX Intracellular delivery; transfection agent; cancer; infectious disease;
KW peptide vector.
XX
OS Synthetic.
XX
FN WC200210201-A2.

XX 07-FEB-2002.
PD
XX
PF 26-JUL-2001; 2001WO-US023406.
XX
PR 31-JUL-2000; 2000US-0221932P.
XX
PA (ACTI-) ACTIVE MOTIF.
PA (CNRS) CENT NAT RECH SCI.
XX
PI Divida G, Morris M, Mery J, Heitz F, Fernandez J, Archdeacon J;
PI Horndorp K;
XX
DR WPI; 2002-329441/36.
XX
PT Transfection agent that comprises a peptide comprising hydrophobic and
PT hydrophilic domain and having amino acid residues of specified length is
PT useful for a non-covalent association with and transport of a
PT heterologous compound into a cell.
XX
PS Claim 12; Page 17; 156pp; English.
XX
CC The invention relates to a transfection agent comprises a peptide of
CC about 16 - 30 amino acids in length. Peptides of the invention comprise a
CC hydrophobic domain, a hydrophilic domain, optionally a spacer sequence
CC between the domains and a functional group conjugated to at least one
CC terminal of the peptide. Peptides of the invention are useful for a non-
CC covalent association with and transport of a heterologous compound into a
CC cell. They are also useful for promoting the cellular internalisation of
CC at least one member e.g. peptide, proteins, antibodies, their derivatives
CC and/or conjugates. They may form part of a pharmaceutical composition to
CC deliver the compound selected from a diagnostic or therapeutic compound,
CC to treat at least one condition such as cancer or an infectious disease,
CC or which targets a cancerous cell or pathogen-infected cell and to
CC deliver a peptide or inhibitor that disrupts the activity of the enzyme.
CC The agent of the invention has a transfection efficiency of at least 5%
CC for at least two of the members of the group of the compounds. The agent
CC has a good delivery efficiency for a broad spectrum of compounds and cell
CC types, has a low toxicity, are easy to handle and easy to formulate in
CC conjunction with the many different compound types that it can deliver.
CC The peptides are serum sensitive, thus they bode particularly well for
CC systemic and/or localised in patients. The current sequence represents
CC the peptide transfection agent Pep-2.2
XX
SQ Sequence 20 AA;

Query Match 100.0%; Score 123; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KEIWWETWWTEASQPKRKV 20
| | | | | | | | | | | | | | | |
Db 1 KEIWWETWWTEASQPKRKV 20

Search completed: March 1, 2004, 16:55:55
Job time : 53.0189 secs

OM protein - protein search, using sw model
Run on: March 1, 2004, 16:46:26 ; Search time 13.1132 Seconds
(without alignments)
146.709 Million cell updates/sec

Title: US-09-915-914B-9
Perfect score: 123
Sequence: 1 KETWETWTEASQPKRKV 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78: +
1: pir1: +
2: pir2: +
3: pir3: +
4: pir4: +

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57.5	46.7	559	2 B47175	reverse transcript
2	57.5	46.7	1003	1 GNWLV	HIV-1 retropepsin
3	57.5	46.7	1003	1 B4001	HIV-1 retropepsin
4	57.5	46.7	1003	2 T09440	pol polyprotein -
5	57.5	46.7	1012	1 GNWVL	HIV-1 retropepsin
6	57.5	46.7	1015	1 GNWH3	HIV-1 retropepsin
7	52.5	42.7	902	2 T01668	pol polyprotein -
8	52.5	42.7	1002	2 S54378	pol polyprotein -
9	52	42.3	413	2 C91229	hypothetical prote
10	52	42.3	413	2 B86076	hypothetical prote
11	52	42.3	418	2 S40824	hypothetical 48K p
12	51.5	41.9	1002	1 GNLJND	HIV-1 retropepsin
13	51	41.5	849	2 D82510	chitinase VCA0027

hypothetical prote
hypothetical prote
probable transcrip
hypothetical prote
spindolin-related
ethylene-insensiti
hypothetical prote
reverse transcript
hypothetical prote
pol polyprotein -
HIV-1 retropepsin
hypothetical prote
probable membrane
probable hydrolase
hypothetical prote
hypothetical prote
plus fringe glycop
homeotic protein C
homeotic protein C
conserved hypothet
hypothetical prote
conserved hypothet
chloride peroxidas
hypothetical prote
MFS permease limpo
acetylactate synth
probable transport
large T antigen -
poly-beta-hydroxyb
hypothetical prote
callose synthase c
hypothetical prote

14 49 39.8 463 2 T48116
15 48 39.0 1143 2 T22952
16 47 38.2 197 2 F70622
17 47 38.2 305 2 A83340
18 47 38.2 402 2 F82495
19 47 38.2 567 2 E96764
20 46.5 37.8 111 2 AH2530
21 46.5 37.8 559 2 A47175
22 46.5 37.8 894 2 T27007
23 46.5 37.8 912 2 S33980
24 46.5 37.8 1003 1 GNVWA2
25 46 37.4 269 2 E83405
26 46 37.4 451 2 T37833
27 46 37.4 507 2 T35677
28 46 37.4 563 2 B70918
29 46 37.4 710 2 T25734
30 46 37.4 823 2 T08092
31 45.5 37.0 862 2 B53689
32 45.5 37.0 1332 1 I48314
33 45 36.6 130 2 A82599
34 45 36.6 178 2 H83349
35 45 36.6 211 2 D69529
36 45 36.6 321 1 A28557
37 45 36.6 334 2 T49195
38 45 36.6 535 2 AE2710
39 45 36.6 573 1 C64131
40 45 36.6 583 2 F97492
41 45 36.6 586 1 TVVPBP
42 45 36.6 619 2 AH2773
43 45 36.6 637 2 F97553
44 45 36.6 1963 2 T49914
45 44.5 36.2 226 2 T20645

Search completed: March 1, 2004, 19:34:33
Job time : 15.2041 secs

OM protein - protein search, using sw model

Run on: March 1, 2004, 16:39:39 ; Search time 8.11321 Seconds
(without alignments)
128.359 Million cell updates/sec

Title: US-09-915-914B-9
Perfect score: 123
Sequence: 1 KETWETWTEASQPKRKV 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57.5	46.7	1003	1	POL_HV1H2 P04585 human immun
2	57.5	46.7	1003	1	POL_HV1Y2 P35963 human immun
3	57.5	46.7	1006	1	POL_HV1MN P05961 human immun
4	57.5	46.7	1007	1	POL_HV1JR P20875 human immun
5	57.5	46.7	1015	1	POL_HV1B1 P03366 human immun
6	57.5	46.7	1015	1	POL_HV1B5 P04587 human immun
7	57.5	46.7	1015	1	POL_HV1BR P03367 human immun
8	57.5	46.7	1015	1	POL_HV1PV P03368 human immun
9	52.5	42.7	1002	1	POL_HV1EL P04589 human immun
10	52.5	42.7	1002	1	POL_HV1MA P04588 human immun
11	52.5	42.7	1002	1	POL_HV1RH P05959 human immun
12	52.5	42.7	1002	1	POL_HV1Z2 P12499 human immun
13	52.5	42.7	1003	1	POL_HV1N5 P12497 human immun
14	52.5	42.7	1003	1	POL_HV1OY P20892 human immun
15	52	42.3	413	1	YIHS_ECOLI P32140 escherichia
16	51.5	41.9	1002	1	POL_HV1ND P18802 human immun
17	47	38.2	567	1	EILJ_ARATH O23116 arabidopsis

18	46.5	37.8	1002	1	POL_HV1U4 P24740 human immun
19	46.5	37.8	1003	1	POL_HV1A2 P03369 human immun
20	46	37.4	78	1	Y009_BPL2 P42544 bacterioph
21	46	37.4	628	1	EIN3_ARATH O24606 arabidopsis
22	45.5	37.0	860	1	LOXA_LYCES P38415 lycopersico
23	45.5	37.0	862	1	CUT1_RAT P53565 rattus norv
24	45.5	37.0	1395	1	CUT1_MOUSE P53564 mus musculu
25	45	36.6	176	1	CYT1_STOHE P81662 stoichactis
26	45	36.6	211	1	YM36_ARCFU O28047 archaeoglob
27	45	36.6	373	1	PRXC_CALFU P04963 caldariomyc
28	45	36.6	518	1	EIL2_ARATH O23115 arabidopsis
29	45	36.6	573	1	ILV1_HAEIN P45261 haenophilus
30	45	36.6	586	1	TALA_POVBO P24851 bovine poly
31	45	36.6	1136	1	NCS2_CHICK Q90703 gallus gall
32	45	36.6	1559	1	STCJ_EMENI Q00681 emerice
33	44.5	36.2	861	1	LOX1_SOLFU P37831 solanum tub
34	44	35.8	400	1	GUN5_BACAG O85465 bacillus ag
35	44	35.8	409	1	GUN2_BACS4 P06565 bacillus sp
36	44	35.8	485	1	RT16_MYXXA P23072 myxococcus
37	44	35.8	488	1	GUN1_BACS4 P06566 bacillus sp
38	44	35.8	565	1	MOBA_BIFLO Q8gn32 bifidobacte
39	44	35.8	964	1	RRPO_MCMV P11640 maize chlor
40	44	35.8	1019	1	POL_SIVS4 P12502 simian immu
41	44	35.8	1022	1	POL_SIVSP P19505 simian immu
42	44	35.8	1054	1	POL_SIVMK P05897 simian immu
43	44	35.8	1056	1	POL_SIVM1 P05896 simian immu
44	44	35.8	1171	1	ZBE4_HUMAN O75132 homo sapien
45	44	35.8	1196	1	XPG_XENLA P14629 xenopus lae

Search completed: March 1, 2004, 19:25:05

Job time : 9.11321 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:40:39 ; Search time 37.4528 Seconds
(without alignments)
168.488 Million cell updates/sec

Title: US-09-915-914B-9
Perfect score: 123
Sequence: 1 KETWETWTEASQPKRKV 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
------------	-------	-------------	--------	----	-------------

1	64	52.0	793	17	Q8TVU1	Q8tvul methanopyru
2	60.5	49.2	433	15	Q79787	Q79787 human immu
3	60.5	49.2	1433	15	Q8AE56	Q8ae56 human immu
4	60	48.8	281	16	Q7U8T9	Q7u8t9 synchococc
5	59	48.0	66	5	Q9BPC0	Q9bpc0 conus tessu
6	57.5	46.7	212	15	Q9WGU7	Q9wgu7 human immu
7	57.5	46.7	225	15	Q998V3	Q998v3 human immu
8	57.5	46.7	236	15	Q9WGX3	Q9wgx3 human immu
9	57.5	46.7	237	15	Q9WGV0	Q9wgv0 human immu
10	57.5	46.7	237	15	Q9WGV3	Q9wgv3 human immu
11	57.5	46.7	237	15	Q9WGV7	Q9wgv7 human immu
12	57.5	46.7	237	15	Q9WGW5	Q9wgw5 human immu
13	57.5	46.7	237	15	Q9WGW0	Q9wgw0 human immu
14	57.5	46.7	237	15	Q9WGV5	Q9wgv5 human immu
15	57.5	46.7	237	15	Q9WGV9	Q9wgv9 human immu
16	57.5	46.7	237	15	Q9W8H5	Q9w8h5 human immu
17	57.5	46.7	237	15	Q9W9U0	Q9w9u0 human immu
18	57.5	46.7	237	15	Q9WGX6	Q9wgx6 human immu
19	57.5	46.7	237	15	Q9WGW2	Q9wgw2 human immu
20	57.5	46.7	237	15	Q9WGX5	Q9wgx5 human immu
21	57.5	46.7	237	15	Q9WGW1	Q9wgw1 human immu
22	57.5	46.7	237	15	Q9WGV2	Q9wgv2 human immu
23	57.5	46.7	237	15	Q9WGU8	Q9wgu8 human immu
24	57.5	46.7	237	15	Q9WGW6	Q9wgw6 human immu
25	57.5	46.7	237	15	Q9WGV6	Q9wgv6 human immu
26	57.5	46.7	237	15	Q9WGV8	Q9wgv8 human immu
27	57.5	46.7	237	15	Q9WGW3	Q9wgw3 human immu
28	57.5	46.7	237	15	Q9WGW4	Q9wgw4 human immu
29	57.5	46.7	237	15	Q9WGV1	Q9wgv1 human immu
30	57.5	46.7	237	15	Q9WGV4	Q9wgv4 human immu
31	57.5	46.7	514	15	Q9DLJ8	Q9dlj8 human immu
32	57.5	46.7	519	15	Q9IDI3	Q9idi3 human immu
33	57.5	46.7	523	15	Q9IDI9	Q9idi9 human immu
34	57.5	46.7	523	15	Q9IDC7	Q9idc7 human immu
35	57.5	46.7	523	15	Q9IDB6	Q9idb6 human immu
36	57.5	46.7	523	15	Q9IDB2	Q9idb2 human immu
37	57.5	46.7	523	15	Q9IDF2	Q9idf2 human immu
38	57.5	46.7	523	15	Q9IDB0	Q9idb0 human immu
39	57.5	46.7	524	15	Q9IDJ7	Q9idj7 human immu
40	57.5	46.7	524	15	Q9IDI8	Q9idi8 human immu
41	57.5	46.7	524	15	Q9IDI7	Q9idi7 human immu
42	57.5	46.7	524	15	Q9IDD1	Q9idd1 human immu
43	57.5	46.7	524	15	Q9IDI6	Q9idi6 human immu
44	57.5	46.7	524	15	Q9IDB8	Q9idb8 human immu
45	57.5	46.7	524	15	Q9IDI2	Q9idi2 human immu

Search completed: March 1, 2004, 19:31:58
Job time : 37.4528 secs

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OM protein - protein search, using sw model

Run on: March 1, 2004, 13:31:13 ; Search time 55.6698 Seconds
(without alignments)
106.584 Million cell updates/sec

Title: US-09-915-914B-10
Perfect score: 135
Sequence: 1 KETWETWETWSQPKKRV 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Match	Length DB	ID	Description
1	135	100.0	21	5 ABB77674	Abb77674 Peptide t
2	123	91.1	21	5 ABG78995	Abg78995 Cell pene
3	123	91.1	21	5 ABB77693	Abb77693 Peptide t
4	123	91.1	21	5 ABB77671	Abb77671 Peptide t
5	123	91.1	21	7 ADB68484	Adb68484 Peptide s
6	123	91.1	21	7 ADC22460	Adc22460 Protein-d
7	120	88.9	19	5 ABB77676	Abb77676 Peptide t
8	117.5	87.0	20	5 ABB77694	Abb77694 Peptide t
9	111	82.2	19	5 ABB10106	Abb10106 Peptide t

10	108	80.0	19	5 ABB77675	Abb77675 Peptide t
11	108	80.0	20	5 ABB77672	Abb77672 Peptide t
12	97	71.9	19	5 ABB77699	Abb77699 Peptide t
13	94	69.6	20	5 ABB77673	Abb77673 Peptide t
14	90	66.7	21	5 ABB77678	Abb77678 Generic p
15	78	57.8	12	5 ABB77689	Abb77689 Hydrophob
16	78	57.8	12	5 ABP56174	Abp56174 Cell-targ
17	78	57.8	26	5 ABP56200	Abp56200 Chimeric
18	74	54.8	19	5 ABB77670	Abb77670 Peptide t
19	69	51.1	11	5 ABB77695	Abb77695 Peptide t
20	63	46.7	17	5 ABB77667	Abb77667 Peptide t
21	62	45.9	286	3 AAG54774	Aag54774 Arabidops
22	62	45.9	383	3 AAG42073	Aag42073 Arabidops
23	62	45.9	432	3 AAG42072	Aag42072 Arabidops
24	62	45.9	435	3 AAG42071	Aag42071 Arabidops
25	59	43.7	9	5 ABB77692	Abb77692 Peptide t
26	59	43.7	18	5 ABB77666	Abb77666 Peptide t
27	59	43.7	19	5 ABB77668	Abb77668 Peptide t
28	59	43.7	19	5 ABB77698	Abb77698 Peptide t
29	59	43.7	19	5 ABB77669	Abb77669 Peptide t
30	59	43.7	20	5 ABB77679	Abb77679 Generic p
31	57.5	42.6	20	2 AAR57412	Aar57412 Peptide f
32	57.5	42.6	89	5 ABR40497	Abr40497 Human sec
33	57.5	42.6	89	5 ABR40420	Abr40420 Human sec
34	57	42.2	418	3 AAB35809	Aab35809 Mannose i
35	57	42.2	496	4 ABG25893	Abg25893 Novel hum
36	57	42.2	928	4 ABG30068	Abg30068 Novel hum
37	57	42.2	928	4 ABG29926	Abg29926 Novel hum
38	56	41.5	10	5 ABB77696	Abb77696 Peptide t
39	56	41.5	16	2 AAW91048	Aaw91048 Internali
40	56	41.5	16	3 AAB27062	Aab27062 Beta-cate
41	56	41.5	16	3 AAB35696	Aab35696 Peptide a
42	56	41.5	16	3 AAB03929	Aab03929 Internali
43	56	41.5	27	5 ABG78990	Abg78990 Cell pene
44	56	41.5	27	5 AAU78348	Aau78348 Signal se
45	56	41.5	27	5 ABG75506	Abg75506 Signal-se

ALIGNMENTS

RESULT 1
ABB77674
ID ABB77674 standard; peptide; 21 AA.
XX
AC ABB77674;
XX
DT 01-JUL-2002 (first entry)
XX
DE Peptide transfection agent Pep-2.3.
XX
KW Intracellular delivery; transfection agent; cancer; infectious disease;
KW peptide vector.
XX
OS Synthetic.
XX
PN WO200210201-A2.

XX

07-FEB-2002.

PD

26-JUL-2001; 2001WO-US023406.

XX

31-JUL-2000; 2000US-0221932P.

XX

(ACTI-) ACTIVE MOTIF.

(CNRS) CENT NAT RECH SCI.

XX

Divida G, Morris M, Mery J, Heitz F, Fernandez J, Archdeacon J;

Horndorp K;

PI

WPI; 2002-329441/36.

XX

Transfection agent that comprises a peptide comprising hydrophobic and hydrophilic domain and having amino acid residues of specified length is useful for a non-covalent association with and transport of a heterologous compound into a cell.

XX

Claim 12; Page 17; 156pp; English.

PS

The invention relates to a transfection agent comprises a peptide of about 16 - 30 amino acids in length. Peptides of the invention comprise a hydrophobic domain, a hydrophilic domain, optionally a spacer sequence between the domains and a functional group conjugated to at least one terminal of the peptide. Peptides of the invention are useful for a non-covalent association with and transport of a heterologous compound into a cell. They are also useful for promoting the cellular internalisation of at least one member e.g. peptide, proteins, antibodies, their derivatives and/or conjugates. They may form part of a pharmaceutical composition to deliver the compound selected from a diagnostic or therapeutic compound, to treat at least one condition such as cancer or an infectious disease, or which targets a cancerous cell or pathogen-infected cell and to deliver a peptide or inhibitor that disrupts the activity of the enzyme. The agent of the invention has a transfection efficiency of at least 5% for at least two of the members of the group of the compounds. The agent has a good delivery efficiency for a broad spectrum of compounds and cell types, has a low toxicity, are easy to handle and easy to formulate in conjunction with the many different compound types that it can deliver. The peptides are serum sensitive, thus they bode particularly well for systemic and/or localised in patients. The current sequence represents the peptide transfection agent Pep-2.3

XX

Sequence 21 AA;

SQ

Query Match 100.0%; Score 135; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 KETWETWETWSQPKKKRV 21

|||||

Db

1 KETWETWETWSQPKKKRV 21

Search completed: March 1, 2004, 16:55:57

Job time : 57.6698 secs

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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:46:26 ; Search time 13.7689 Seconds
(without alignments)
146.709 Million cell updates/sec

Title: US-09-915-914B-10

Perfect score: 135

Sequence: 1 KETWETWETWSQPKKKRV 21

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	58.5	43.3	688	1 TVWPTJ	large T antigen -
2	58	43.0	691	1 TWPAS	large T antigen -
3	58	43.0	695	1 TVVPTB	large T antigen -
4	57	42.2	418	2 S40824	hypothetical 48K p
5	56.5	41.9	894	2 T27007	hypothetical prote
6	54.5	40.4	708	1 TVVPT4	large T antigen -
7	54	40.0	374	2 AG0937	hypothetical prote
8	54	40.0	413	2 C91229	hypothetical prote
9	54	40.0	413	2 B86076	hypothetical prote
10	51	37.8	435	2 D71857	hypothetical prote
11	51	37.8	435	2 B64658	hypothetical prote
12	51	37.8	519	2 E82932	spermidine/putresc
13	51	37.8	559	2 B47175	reverse transcript

14 51 37.8 965 2 JQ0058
15 51 37.8 1002 1 GNLDND
16 51 37.8 1002 2 S54378
17 51 37.8 1003 1 GNVWL
18 51 37.8 1003 1 B4001
19 51 37.8 1003 2 T09440
20 51 37.8 1012 1 GNVWL
21 51 37.8 1015 1 GNVWH3
22 50.5 37.4 1451 2 B86286
23 50.5 37.4 1469 2 H96622
24 50 37.0 455 2 T48973
25 49 36.3 200 2 T42547
26 49 36.3 264 2 F71466
27 49 36.3 629 2 T05089
28 48.5 35.9 188 2 A75382
29 48.5 35.9 239 2 C84505
30 48.5 35.9 331 2 A61046
31 48.5 35.9 472 2 T41684
32 48.5 35.9 692 2 H70362
33 48.5 35.9 770 2 S75042
34 48.5 35.9 794 2 S50687
35 48.5 35.9 1032 2 S12153
36 48.5 35.9 1034 1 GNLDCA
37 48.5 35.9 1035 1 GNLDGG
38 48.5 35.9 1036 1 GNLDJG
39 48.5 35.9 1055 1 GNLDJT
40 48 35.6 45 2 C82233
41 48 35.6 338 2 A82890
42 48 35.6 486 2 F64204
43 48 35.6 586 1 TVPBP
44 48 35.6 652 2 T34497
45 48 35.6 935 2 T48778

hypothetical 11k
HIV-1 retropepsin
pol polyprotein -
HIV-1 retropepsin
HIV-1 retropepsin
pol polyprotein -
HIV-1 retropepsin
HIV-1 retropepsin
F9L1.15 protein -
probable ABC trans
cytochrome P450-li
gene 4 protein - e
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
ecdysone-induced m
probable sterol o-
glycogen phosphory
hypothetical prote
hypothetical prote
pol polyprotein -
HIV-1 retropepsin
HIV-1 retropepsin
HIV-1 retropepsin
hypothetical prote
hypothetical prote
spermidine/putresc
large T antigen -
hypothetical prote
hypothetical prote

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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:39:39 ; Search time 8.51887 Seconds
(without alignments)
128.359 Million cell updates/sec

Title: US-09-915-914B-10
Perfect score: 135
Sequence: 1 KETWETWETWSQPKKRRKV 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Search completed: March 1, 2004, 19:34:34

Job time : 14.8398 secs

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58.5	43.3	688	1 TALA_POVJC	P03072 polyomaviru
2	58	43.0	691	1 TALA_POVBA	P14999 polyomaviru
3	58	43.0	695	1 TALA_POVBK	P03071 polyomaviru
4	57	42.2	413	1 YIHS_ECOLI	P32140 escherichia
5	54.5	40.4	708	1 TALA_SV40	P03070 simian viru
6	51	37.8	964	1 RPPO_MCV	P11640 maize chlor
7	51	37.8	1002	1 POL_HVIEL	P04589 human immun
8	51	37.8	1002	1 POL_HVIND	P18802 human immun
9	51	37.8	1002	1 POL_HVIZ2	P12499 human immun
10	51	37.8	1003	1 POL_HV1H2	P04585 human immun
11	51	37.8	1003	1 POL_HV1Y2	P35963 human immun
12	51	37.8	1007	1 POL_HV1JR	P20875 human immun
13	51	37.8	1015	1 POL_HV1B1	P03366 human immun
14	51	37.8	1015	1 POL_HV1B5	P04587 human immun
15	51	37.8	1015	1 POL_HV1BR	P03367 human immun
16	51	37.8	1015	1 POL_HV1PV	P03368 human immun
17	50	37.0	1006	1 POL_HV1MN	P05961 human immun

18 48.5 35.9 692 1 PHSG_AQUAE
19 48.5 35.9 794 1 YE14_YEAST
20 48.5 35.9 1034 1 POL_HV2CA
21 48.5 35.9 1035 1 POL_HV2KR
22 48.5 35.9 1035 1 POL_HV2NZ
23 48.5 35.9 1035 1 POL_HV2SB
24 48.5 35.9 1036 1 POL_HV2RO
25 48.5 35.9 1049 1 POL_HV2G1
26 48.5 35.9 1055 1 POL_HV2ST
27 48.5 35.9 1073 1 POL_HV2D1
28 48.5 35.9 1142 1 POL_HV2BE
29 48 35.6 41 1 LPW_VIEPA
30 48 35.6 176 1 CYTI_STOHE
31 48 35.6 559 1 POTA_MYCGE
32 48 35.6 586 1 TALA_POVBO
33 47.5 35.2 355 1 HKN1_LYCES
34 47.5 35.2 398 1 HKL1_ARATH
35 47.5 35.2 1585 1 YQBO_BACSU
36 47 34.8 336 1 SIFA_SALTY
37 47 34.8 504 1 MATK_NEPAL
38 47 34.8 506 1 MATK_CALVU
39 47 34.8 508 1 MATK_LOTJA
40 47 34.8 560 1 POTA_MYCPN
41 46.5 34.4 315 1 SECF_SYNY3
42 46.5 34.4 568 1 PHAC_CHRVO
43 46 34.1 200 1 UL55_HSVEB
44 46 34.1 502 1 MATK_VACVI
45 46 34.1 508 1 MATK_LOTPU

O66932 aquifex aeo
P39961 saccharomyc
P24107 human immu
Q74120 human immu
P05962 human immu
P12451 human immu
P04584 human immu
P18042 human immu
P20876 human immu
P17757 human immu
P18096 human immu
P22100 vibrio para
P81662 stoichactis
P47288 mycoplasma
P24851 bovine poly
Q41330 lycopersico
P46639 arabidopsis
P45931 bacillus su
Q56061 salmonella
Q95gt2 nepenthes a
Q47143 calluna vul
Q9bbu2 lotus japon
P75059 mycoplasma
Q55611 synechocyst
Q9zhi2 chromobacte
P28963 equine herp
Q8wif9 vaccinium v
Q9tkp8 lotus pursh

Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archheap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query				DB	ID	Description
	No.	Score	Match	Length			
1	63	46.7	793	17	Q8TVU1	Q8tvu1	methanopyru
2	61	45.2	431	10	Q8H8C6	Q8h8c6	oryza sativ
3	58.5	43.3	688	12	Q91DF4	Q91df4	polyomaviru
4	58.5	43.3	688	12	Q8JUC5	Q8juc5	polyomaviru
5	58.5	43.3	688	12	Q8JUD5	Q8jud5	polyomaviru
6	58.5	43.3	688	12	Q9WM07	Q9wm07	polyomaviru
7	58.5	43.3	688	12	Q8V6G6	Q8v6g6	polyomaviru
8	58.5	43.3	688	12	Q8JWJ4	Q8jwj4	polyomaviru
9	58.5	43.3	688	12	Q9WM08	Q9wm08	polyomaviru
10	58.5	43.3	688	12	Q91DF8	Q91df8	polyomaviru
11	58.5	43.3	688	12	Q8JUD8	Q8jud8	polyomaviru
12	58.5	43.3	688	12	P88898	P88898	polyomaviru
13	58.5	43.3	688	12	Q8JUE2	Q8jue2	polyomaviru
14	58.5	43.3	688	12	Q91NL8	Q91nl8	polyomaviru
15	58.5	43.3	688	12	Q91DF5	Q91df5	polyomaviru
16	58.5	43.3	688	12	Q9W8D4	Q9w8d4	polyomaviru
17	58.5	43.3	688	12	Q91NM2	Q91nm2	polyomaviru
18	58.5	43.3	688	12	Q91NL2	Q91nl2	polyomaviru
19	58.5	43.3	688	12	Q8JZK0	Q8jzk0	polyomaviru
20	58.5	43.3	688	12	Q993Y4	Q993y4	polyomaviru
21	58.5	43.3	688	12	Q8V6G3	Q8v6g3	polyomaviru
22	58.5	43.3	688	12	Q9WM10	Q9wm10	polyomaviru

Search completed: March 1, 2004, 19:25:06
Job time : 9.51887 secs

23 58.5 43.3 688 12 Q8JUC9 Q8juc9 polyomaviru
24 58.5 43.3 688 12 Q91DG7 Q91dg7 polyomaviru
25 58.5 43.3 688 12 Q91OD2 Q91od2 polyomaviru
26 58.5 43.3 688 12 Q8JZJ2 Q8jzj2 polyomaviru
27 58.5 43.3 688 12 Q8V6F7 Q8v6f7 polyomaviru
28 58.5 43.3 688 12 Q8JUB9 Q8jub9 polyomaviru
29 58.5 43.3 688 12 Q8JJK3 Q8jjk3 polyomaviru
30 58.5 43.3 688 12 Q9DPC9 Q9dpc9 polyomaviru
31 58.5 43.3 688 12 Q9DUG1 Q9dug1 polyomaviru
32 58.5 43.3 688 12 Q91DE6 Q91de6 polyomaviru
33 58.5 43.3 688 12 Q8JUB1 Q8jub1 polyomaviru
34 58.5 43.3 688 12 Q82950 Q82950 polyomaviru
35 58.5 43.3 688 12 Q8JUB6 Q8jub6 polyomaviru
36 58.5 43.3 688 12 Q8V6H1 Q8v6h1 polyomaviru
37 58.5 43.3 688 12 Q91NLS Q91nl5 polyomaviru
38 58.5 43.3 688 12 Q8V6G7 Q8v6g7 polyomaviru
39 58.5 43.3 688 12 Q9DUG4 Q9dug4 polyomaviru
40 58.5 43.3 688 12 Q8JWJ3 Q8jwj3 polyomaviru
41 58.5 43.3 688 12 Q91DH4 Q91dh4 polyomaviru
42 58.5 43.3 688 12 Q8JWI7 Q8jwi7 polyomaviru
43 58.5 43.3 688 12 Q8JUC2 Q8juc2 polyomaviru
44 58.5 43.3 688 12 Q993Y5 Q993y5 polyomaviru
45 58.5 43.3 688 12 Q8JUE1 Q8jue1 polyomaviru

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QM protein - protein search, using sw model

Run on: March 1, 2004, 13:31:13 ; Search time 50.3679 Seconds
(without alignments)
106.984 Million cell updates/sec

Title: US-09-915-914B-11
Perfect score: 119
Sequence: 1 KETWETWTWSQPKKKRKV 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04: *
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		DB	ID	Description
		Match	Length			
1	119	100.0	19	5	ABB77675	Abb77675 Peptide t
2	108	90.8	21	5	ABB77674	Abb77674 Peptide t
3	102	85.7	21	5	ABG78995	Abg78995 Cell pene
4	102	85.7	21	5	ABB77693	Abb77693 Peptide t
5	102	85.7	21	5	ABB77671	Abb77671 Peptide t
6	102	85.7	21	7	ADB68484	Adb68484 Peptide s
7	102	85.7	21	7	ADC22460	Adc22460 Protein-d
8	93	78.2	19	5	ABB77676	Abb77676 Peptide t
9	90.5	76.1	20	5	ABB77694	Abb77694 Peptide t

Search completed: March 1, 2004, 19:32:02
Job time : 43.3255 secs

10 87 73.1 20 5 ABB77672 Abb77672 Peptide t
11 84 70.6 19 5 ABB10106 Abb10106 Peptide t
12 77 64.7 20 5 ABB77673 Abb77673 Peptide t
13 71 59.7 21 5 ABB77678 Abb77678 Generic p
14 70 58.8 19 5 ABB77699 Abb77699 Peptide t
15 61.5 51.7 11 5 ABB77695 Abb77695 Peptide t
16 61.5 51.7 12 5 ABB77689 Abb77689 Hydrophob
17 61.5 51.7 12 5 ABP56174 Abp56174 Cell-targ
18 61.5 51.7 26 5 ABP56200 Abp56200 Chimeric
19 56 47.1 10 5 ABB77696 Abb77696 Peptide t
20 56 47.1 27 5 ABG78990 Abg78990 Cell pene
21 56 47.1 27 5 AAU78348 Aau78348 Signal se
22 56 47.1 27 5 ABB75506 Abg75506 Signal-se
23 56 47.1 27 5 ABB77685 Abb77685 New pepti
24 56 47.1 27 5 ABB77687 Abb77687 New pepti
25 56 47.1 27 5 ABB81176 Abb81176 Signal se
26 56 47.1 27 5 AAE23685 Aae23685 Fluoresce
27 56 47.1 27 6 ABB82542 Abb82542 Signal se
28 56 47.1 27 6 ABR84443 Abr84443 Chimeric
29 55.5 46.6 17 5 ABB77667 Abb77667 Peptide t
30 54 45.4 115 3 AAB57013 Aab57013 Human pro
31 53.5 45.0 19 5 ABB77670 Abb77670 Peptide t
32 52 43.7 128 3 AAG24065 Aag24065 Arabidops
33 52 43.7 128 3 AAG35083 Aag35083 Arabidops
34 52 43.7 145 3 AAG54796 Aag54796 Arabidops
35 51.5 43.3 9 5 ABB77692 Abb77692 Peptide t
36 51.5 43.3 18 5 ABB77666 Abb77666 Peptide t
37 51.5 43.3 19 5 ABB77668 Abb77668 Peptide t
38 51.5 43.3 19 5 ABB77698 Abb77698 Peptide t
39 51.5 43.3 19 5 ABB77669 Abb77669 Peptide t
40 51.5 43.3 20 5 ABB77679 Abb77679 Generic p
41 51 42.9 20 2 AAR57412 Aar57412 Peptide f
42 51 42.9 27 4 AAB85057 Aab85057 N-termina
43 51 42.9 27 5 ABB78712 Abb78712 Peptide M
44 51 42.9 27 5 ABB77681 Abb77681 Peptide v
45 51 42.9 181 6 ABR41729 Abr41729 Human DIT

ALIGNMENTS

RESULT 1
ABB77675
ID ABB77675 standard; peptide; 19 AA.
XX
AC ABB77675;
XX
DT 01-JUL-2002 (first entry)
XX
DE Peptide transfection agent Pep-2.4.
XX
KW Intracellular delivery; transfection agent; cancer; infectious disease;
KW peptide vector.
XX
OS Synthetic.
XX
PN WC200210201-A2.

XX 07-FEB-2002.
PD
XX
PF 26-JUL-2001; 2001WO-US023406.
XX
PR 31-JUL-2000; 2000US-0221932P.
XX
PA (ACTI-) ACTIVE MOTIF.
PA (CNRS) CENT NAT RECH SCI.
XX
PI Divida G, Morris M, Mery J, Heitz F, Fernandez J, Archdeacon J;
PI Horndorp K;
XX
DR WPI; 2002-329441/36.
XX
PT Transfection agent that comprises a peptide comprising hydrophobic and
PT hydrophilic domain and having amino acid residues of specified length is
PT useful for a non-covalent association with and transport of a
PT heterologous compound into a cell.
XX
PS Claim 12; Page 17; 156pp; English.
XX
CC The invention relates to a transfection agent comprises a peptide of
CC about 16 - 30 amino acids in length. Peptides of the invention comprise a
CC hydrophobic domain, a hydrophilic domain, optionally a spacer sequence
CC between the domains and a functional group conjugated to at least one
CC terminal of the peptide. Peptides of the invention are useful for a non-
CC covalent association with and transport of a heterologous compound into a
CC cell. They are also useful for promoting the cellular internalisation of
CC at least one member e.g. peptide, proteins, antibodies, their derivatives
CC and/or conjugates. They may form part of a pharmaceutical composition to
CC deliver the compound selected from a diagnostic or therapeutic compound,
CC to treat at least one condition such as cancer or an infectious disease,
CC or which targets a cancerous cell or pathogen-infected cell and to
CC deliver a peptide or inhibitor that disrupts the activity of the enzyme.
CC The agent of the invention has a transfection efficiency of at least 5%
CC for at least two of the members of the group of the compounds. The agent
CC has a good delivery efficiency for a broad spectrum of compounds and cell
CC types, has a low toxicity, are easy to handle and easy to formulate in
CC conjunction with the many different compound types that it can deliver.
CC The peptides are serum sensitive, thus they bode particularly well for
CC systemic and/or localised in patients. The current sequence represents
CC the peptide transfection agent Pep-2.4
XX
SQ Sequence 19 AA;

Query Match 100.0%; Score 119; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.4e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KETWWETWTSQPKKKRKV 19
| | | | | | | | | | | | | | | | | | | | | |
Db 1 KETWWETWTSQPKKKRKV 19

Search completed: March 1, 2004, 16:55:58
Job time : 51.3679 secs

OM protein - protein search, using sw model
Run on: March 1, 2004, 16:46:26 ; Search time 12.4575 Seconds
(without alignments)
146.709 Million cell updates/sec

Title: US-09-915-914B-11
Perfect score: 119
Sequence: 1 KETWETWTSQPKKKRV 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.78: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	54	45.4	325	2	JC7560	cellulase (EC 3.2.
2	54	45.4	325	2	G70421	probable endogluc
3	54	45.4	472	2	T41684	probable sterol o-
4	53	44.5	142	2	S28757	cytochrome-c oxida
5	51	42.9	118	1	W4WLB2	E4 protein - bovin
6	51	42.9	298	2	B71872	hypothetical prote
7	51	42.9	368	2	E97198	probable enzyme wi
8	51	42.9	376	1	C64135	ribonucleoside-dip
9	50	42.0	160	2	C69900	hypothetical prote
10	50	42.0	308	2	S58504	reverse transcript
11	49.5	41.6	562	2	S25725	poly(3-hydroxyalka
12	49	41.2	338	2	A82890	hypothetical prote
13	49	41.2	1086	2	T40354	hypothetical prote

14	48.5	40.8	894	2	T27007	hypothetical prote
15	48	40.3	1411	2	T48529	hypothetical prote
16	47.5	39.9	229	2	S60454	glucose starvation
17	47.5	39.9	355	2	T07776	Kn1 like-homeo box
18	47.5	39.9	398	2	D85080	KNAT1 homeobox-lik
19	47.5	39.9	688	1	TVVPTJ	large T antigen -
20	47.5	39.9	692	2	H70362	glycogen phosphory
21	47	39.5	159	2	F83733	hypothetical prote
22	47	39.5	178	2	A69090	conserved hypothet
23	47	39.5	376	2	AH0148	ribonucleoside-dip
24	47	39.5	376	2	G84950	ribonucleoside-dip
25	47	39.5	377	2	D81841	ribonucleoside-dip
26	47	39.5	384	2	G81100	ribonucleoside-dip
27	47	39.5	389	2	D82223	ribonucleoside-dip
28	46.5	39.1	331	2	E82170	peptide ABC transp
29	46	38.7	122	2	S32630	ribonucleoside-dip
30	46	38.7	306	1	W2WLEB	E2 protein - bovin
31	46	38.7	376	1	RDEC2R	ribonucleoside-dip
32	46	38.7	376	2	F91018	ribonucleoside-dip
33	46	38.7	376	2	H85862	ribonucleoside-dip
34	46	38.7	376	2	AD0791	ribonucleoside-dip
35	46	38.7	560	2	T32661	hypothetical prote
36	46	38.7	627	2	A70888	hypothetical prote
37	46	38.7	691	1	TVVPTAS	large T antigen -
38	46	38.7	695	1	TVVPTB	large T antigen -
39	46	38.7	1315	2	T05300	hypothetical prote
40	45.5	38.2	354	1	C37842	cytochrome P450 -
41	45.5	38.2	459	2	AG1987	cytochrome P450 [1
42	45.5	38.2	766	2	S37894	hypothetical prote
43	45	37.8	228	2	AE2173	hypothetical prote
44	45	37.8	247	2	T26688	hypothetical prote
45	45	37.8	669	2	T32512	hypothetical prote

Search completed: March 1, 2004, 19:34:35
Job time : 13.5485 secs

OM protein - protein search, using sw model

Run on: March 1, 2004, 16:39:39 ; Search time 7.70755 Seconds
(without alignments)
128.359 Million cell updates/sec

Title: US-09-915-914B-11
Perfect score: 119
Sequence: 1 KETWETWWSQPKKKRKV 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	44.5	42	1 COX1_MYTED	P41774 mytilus edu
2	51	42.9	112	1 VE4_BPV2	P11301 bovine papi
3	51	42.9	375	1 RIR2_HAEIN	P43755 haemophilus
4	47.5	39.9	355	1 HKM1_LYCES	Q41330 lycopersico
5	47.5	39.9	398	1 HKL1_ARATH	P46639 arabidopsis
6	47.5	39.9	688	1 TALA_POVJC	P03072 polyomaviru
7	47.5	39.9	692	1 PHSG_AQUAE	O66932 aquifex aeo
8	47	39.5	376	1 RIR2_BUCAI	P57275 buchnera ap
9	47	39.5	376	1 RIR2_BUCAP	Q8K9W4 buchnera ap
10	47	39.5	376	1 RIR2_BUCBP	Q89as5 buchnera ap
11	46	38.7	257	1 HIS6_VIBVU	Q8d8q5 vibrio vuln
12	46	38.7	375	1 RIR2_ECOLI	P00453 escherichia
13	46	38.7	375	1 RIR2_SALTY	P37427 salmonella
14	46	38.7	691	1 TALA_POVBA	P14999 polyomaviru
15	46	38.7	695	1 TALA_POVBK	P03071 polyomaviru
16	45.5	38.2	459	1 CPXN_ANASP	P29980 anabaena sp
17	45.5	38.2	766	1 STB6_YEAST	P36085 saccharomyc

18	45	37.8	257	1	HIS6_VIBPA	Q87qk6 vibrio para
19	45	37.8	838	1	KFC2_HUMAN	Q96ac6 homo sapien
20	45	37.8	995	1	SR13_HUMAN	Q9y3m8 homo sapien
21	44.5	37.4	364	1	KNX3_HORVU	Q43484 hordeum vul
22	44.5	37.4	568	1	PHAC_CHRVO	Q9zhi2 chromobacte
23	44.5	37.4	642	1	NA95_MOUSE	Q9r017 mus musculu
24	44.5	37.4	646	1	NA95_HUMAN	Q9ulx6 homo sapien
25	44	37.0	41	1	LPW_VIBPA	P22100 vibrio para
26	44	37.0	124	1	YE22_RHIME	Q92qb2 rhizobium m
27	44	37.0	208	1	SODN_BACCR	Q814i6 bacillus ce
28	44	37.0	406	1	ARG1_HUMAN	Q8n6t3 homo sapien
29	44	37.0	611	1	PHBC_RHIME	P50176 r poly-beta
30	44	37.0	621	1	ULP1_YEAST	Q02724 saccharomyc
31	44	37.0	781	1	TL22_CHICK	Q9dgb6 gallus gall
32	44	37.0	793	1	TL21_CHICK	Q9dd78 gallus gall
33	44	37.0	995	1	SR13_MOUSE	Q923q2 mus musculu
34	44	37.0	1171	1	ZBE4_HUMAN	O75132 homo sapien
35	43.5	36.6	361	1	OSH1_ORYSA	P46609 oryza sativ
36	43.5	36.6	397	1	HKL2_MALDO	O04135 malus domes
37	43.5	36.6	398	1	HKL1_MALDO	O04134 malus domes
38	43	36.1	158	1	SSRP_BIFLO	Q8g540 bifidobacte
39	43	36.1	258	1	HIS6_ECOLI	Q8fg48 escherichia
40	43	36.1	258	1	HIS6_ECOLI	P10373 escherichia
41	43	36.1	258	1	HIS6_KLEOX	P45603 klebsiella
42	43	36.1	311	1	CLN6_HUMAN	Q9nww5 homo sapien
43	43	36.1	406	1	KDC2_HUMAN	Q9y2u9 homo sapien
44	43	36.1	557	1	ACEA_YEAST	P28240 saccharomyc
45	43	36.1	574	1	HEMA_INEMD	P03461 influenza b

Search completed: March 1, 2004, 19:25:08
Job time : 9.70755 secs

OM protein - protein search, using sw model
Run on: March 1, 2004, 16:40:39 ; Search time 35.5802 Seconds
(without alignments)
168.488 Million cell updates/sec

Title: US-09-915-914B-11
Perfect score: 119
Sequence: 1 KETWETWWSQPKKKRV 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

%			
Result	Query		
No.	Score	Match Length	ID Description

1	54	45.4	325	16	067401
2	54	45.4	472	3	Q9UU82
3	53	44.5	49	8	Q9TD66
4	53	44.5	1417	10	Q9FJQ9
5	51	42.9	103	12	Q68355
6	51	42.9	298	16	Q9ZKL2
7	51	42.9	368	16	Q97GE6
8	51	42.9	376	16	Q9CMT9
9	51	42.9	376	16	Q7VXX9
10	50	42.0	98	13	Q8AV25
11	50	42.0	160	16	034637
12	50	42.0	431	10	Q8H8C6
13	50	42.0	452	4	Q9H7M8
14	50	42.0	568	8	Q94Z24
15	50	42.0	1412	10	Q7X6H6
16	49.5	41.6	562	2	Q53049
17	49	41.2	338	16	Q9PQ39
18	49	41.2	391	16	Q8A7H7
19	49	41.2	1086	3	043043
20	48.5	40.8	894	5	Q9U297
21	48	40.3	198	5	Q9VXX2
22	48	40.3	217	10	Q8S6K8
23	48	40.3	244	11	Q9EQF4
24	48	40.3	1408	10	Q9LDE8
25	48	40.3	1411	10	Q9LYG0
26	47.5	39.9	229	10	Q41855
27	47.5	39.9	400	10	Q8S3L9
28	47.5	39.9	400	10	Q8S3M0
29	47.5	39.9	688	12	Q91DF4
30	47.5	39.9	688	12	Q8JUC5
31	47.5	39.9	688	12	Q8JUD5
32	47.5	39.9	688	12	Q9WM07
33	47.5	39.9	688	12	Q8V6G6
34	47.5	39.9	688	12	Q8JWJ4
35	47.5	39.9	688	12	Q9WM08
36	47.5	39.9	688	12	Q91DF8
37	47.5	39.9	688	12	Q8JUD8
38	47.5	39.9	688	12	P88898
39	47.5	39.9	688	12	Q8JUE2
40	47.5	39.9	688	12	Q91NL8
41	47.5	39.9	688	12	Q91DF5
42	47.5	39.9	688	12	Q9W8D4
43	47.5	39.9	688	12	Q91NM2
44	47.5	39.9	688	12	Q91NL2
45	47.5	39.9	688	12	Q8JZK0

Search completed: March 1, 2004, 19:32:05
Job time : 38.5802 secs

OM protein - protein search, using sw model

Run on: March 1, 2004, 13:31:13 ; Search time 50.3679 Seconds
(without alignments)
106.584 Million cell updates/sec

Title: US-09-915-914B-12
Perfect score: 125
Sequence: 1 KMWETWETWSQPKKKRKV 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	125	100.0	19	5 ABB77676	Abb77676 Peptide t
2	120	96.0	21	5 ABB77674	Abb77674 Peptide t
3	108	86.4	21	5 ABG78995	Abg78995 Cell pene
4	108	86.4	21	5 ABB77693	Abb77693 Peptide t
5	108	86.4	21	5 ABB77671	Abb77671 Peptide t
6	108	86.4	21	7 ADB68484	Adb68484 Peptide s
7	108	86.4	21	7 ADC22460	Adc22460 Protein-d
8	105	84.0	19	5 ABB10106	Abb10106 Peptide t
9	102.5	82.0	20	5 ABB77694	Abb77694 Peptide t

10	93	74.4	19	5 ABB77675	Abb77675 Peptide t
11	93	74.4	20	5 ABB77672	Abb77672 Peptide t
12	91	72.8	19	5 ABB77699	Abb77699 Peptide t
13	86	68.8	21	5 ABB77678	Abb77678 Generic p
14	79	63.2	20	5 ABB77673	Abb77673 Peptide t
15	64	51.2	19	5 ABB77670	Abb77670 Peptide t
16	63	50.4	12	5 ABB77689	Abb77689 Hydrophob
17	63	50.4	12	5 ABP56174	Abp56174 Cell-targ
18	63	50.4	26	5 ABP56200	Abp56200 Chimeric
19	61	48.8	16	2 AAW91048	Aaw91048 Internali
20	61	48.8	16	3 AAB27062	Aab27062 Beta-cate
21	61	48.8	16	3 AAB35696	Aab35696 Peptide a
22	61	48.8	16	3 AAB03929	Aab03929 Internali
23	57.5	46.0	11	2 AAR57411	Aar57411 Peptide f
24	57	45.6	18	1 AAP90325	Aap90325 Alpha-hel
25	57	45.6	398	4 ABB63456	Abb63456 Drosophil
26	56	44.8	10	5 ABB77696	Abb77696 Peptide t
27	56	44.8	27	5 ABG78990	Abg78990 Cell pene
28	56	44.8	27	5 AAU78348	Aau78348 Signal se
29	56	44.8	27	5 ABG75506	Abg75506 Signal-se
30	56	44.8	27	5 ABB77685	Abb77685 New pepti
31	56	44.8	27	5 ABB77687	Abb77687 New pepti
32	56	44.8	27	5 ABB81176	Abb81176 Signal se
33	56	44.8	27	5 AAE23685	Aae23685 Fluoresce
34	56	44.8	27	6 ABB82542	Abb82542 Signal se
35	56	44.8	27	6 ABR84443	Abr84443 Chimeric
36	55	44.0	16	2 AAW33415	Aaw33415 Trp,Arg a
37	55	44.0	16	6 AAE33896	Aae33896 Drosophil
38	55	44.0	16	6 AAO16668	Aac16668 Cell-perm
39	55	44.0	298	4 ABB03815	Abb03815 Human mus
40	55	44.0	298	4 AAM42405	Aam42405 Human pol
41	55	44.0	298	4 AAU87135	Aau87135 Novel cen
42	55	44.0	298	6 ABU13109	Abu13109 Novel hum
43	54.5	43.6	136	4 AAB66213	Aab66213 SV40 T an
44	54.5	43.6	708	2 AAY06547	Aay06547 SV40 larg
45	54.5	43.6	708	6 ABR55311	Abf55311 Amino aci

ALIGNMENTS

RESULT 1
ABB77676
ID ABB77676 standard; peptide; 19 AA.

XX	AC	ABB77676;
XX	DT	01-JUL-2002 (first entry)
XX	XX	Peptide transfection agent Pep-2.5.
DE	XX	Intracellular delivery; transfection agent; cancer; infectious disease;
KW	XX	peptide vector.
OS	XX	Synthetic.
PN	XX	WO200210201-A2.

XX 07-FEB-2002.
PD
XX
XX AC 26-JUL-2001; 2001WO-US023406.
PF
XX
XX DT 31-JUL-2000; 2000US-0221932P.
PR
XX
XX (ACTI-) ACTIVE MOTIF.
PA (CNRS) CENT NAT RECH SCI.
PI
XX Divida G, Morris M, Mery J, Heitz F, Fernandez J, Archdeacon J;
PI Horndorp K;
XX
XX WPI; 2002-329441/36.
DR
XX
XX Transfection agent that comprises a peptide comprising hydrophobic and
PT hydrophilic domain and having amino acid residues of specified length is
PT useful for a non-covalent association with and transport of a
PT heterologous compound into a cell.
XX
XX Claim 12; Page 17; 156pp; English.
PS
XX The invention relates to a transfection agent comprises a peptide of
CC about 16 - 30 amino acids in length. Peptides of the invention comprise a
CC hydrophobic domain, a hydrophilic domain, optionally a spacer sequence
CC between the domains and a functional group conjugated to at least one
CC terminal of the peptide. Peptides of the invention are useful for a non-
CC covalent association with and transport of a heterologous compound into a
CC cell. They are also useful for promoting the cellular internalisation of
CC at least one member e.g. peptide, proteins, antibodies, their derivatives
CC and/or conjugates. They may form part of a pharmaceutical composition to
CC deliver the compound selected from a diagnostic or therapeutic compound,
CC to treat at least one condition such as cancer or an infectious disease,
CC or which targets a cancerous cell or pathogen-infected cell and to
CC deliver a peptide or inhibitor that disrupts the activity of the enzyme.
CC The agent of the invention has a transfection efficiency of at least 5%
CC for at least two of the members of the group of the compounds. The agent
CC has a good delivery efficiency for a broad spectrum of compounds and cell
CC types, has a low toxicity, are easy to handle and easy to formulate in
CC conjunction with the many different compound types that it can deliver.
CC The peptides are serum sensitive, thus they bode particularly well for
CC systemic and/or localised in patients. The current sequence represents
CC the peptide transfection agent Pep-2.5
XX
SQ Sequence 19 AA;
Query Match 100.0%; Score 125; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KWWETWWTWSQPKKKRV 19
| | | | | | | | | | | | | | | | | | | | | |
Db 1 KWWETWWTWSQPKKKRV 19
RESULT 2
ABB77674

ID ABB77674 standard; peptide; 21 AA.
XX
XX AC ABB77674;
XX
XX DT 01-JUL-2002 (first entry)
XX
XX DE Peptide transfection agent Pep-2.3.
XX
XX KW Intracellular delivery; transfection agent; cancer; infectious disease;
KW peptide vector.
XX
XX OS Synthetic.
XX
XX PN WO200210201-A2.
XX
XX PD 07-FEB-2002.
XX
XX PF 26-JUL-2001; 2001WO-US023406.
XX
XX PR 31-JUL-2000; 2000US-0221932P.
XX
XX PA (ACTI-) ACTIVE MOTIF.
PA (CNRS) CENT NAT RECH SCI.
XX Divida G, Morris M, Mery J, Heitz F, Fernandez J, Archdeacon J;
PI Horndorp K;
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XX WPI; 2002-329441/36.
XX
XX Transfection agent that comprises a peptide comprising hydrophobic and
PT hydrophilic domain and having amino acid residues of specified length is
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XX Claim 12; Page 17; 156pp; English.
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CC between the domains and a functional group conjugated to at least one
CC terminal of the peptide. Peptides of the invention are useful for a non-
CC covalent association with and transport of a heterologous compound into a
CC cell. They are also useful for promoting the cellular internalisation of
CC at least one member e.g. peptide, proteins, antibodies, their derivatives
CC and/or conjugates. They may form part of a pharmaceutical composition to
CC deliver the compound selected from a diagnostic or therapeutic compound,
CC to treat at least one condition such as cancer or an infectious disease,
CC or which targets a cancerous cell or pathogen-infected cell and to
CC deliver a peptide or inhibitor that disrupts the activity of the enzyme.
CC The agent of the invention has a transfection efficiency of at least 5%
CC for at least two of the members of the group of the compounds. The agent
CC has a good delivery efficiency for a broad spectrum of compounds and cell
CC types, has a low toxicity, are easy to handle and easy to formulate in
CC conjunction with the many different compound types that it can deliver.
CC The peptides are serum sensitive, thus they bode particularly well for
CC systemic and/or localised in patients. The current sequence represents
CC the peptide transfection agent Pep-2.3

XX

SQ Sequence 21 AA;

Query Match 96.0%; Score 120; DB 5; Length 21;
Best Local Similarity 100.0%; Pred.No. 1.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WWETWETWSQPKKKRV 19
|||||
Db 4 WWETWETWSQPKKKRV 21

Search completed: March 1, 2004, 16:56:00
Job time : 52.3679 secs

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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:46:26 ; Search time 12.4575 Seconds
(without alignments)
146.709 Million cell updates/sec

Title: US-09-915-914B-12
Perfect score: 125
Sequence: 1 KWWETWETWSQPKKKRV 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:
1: pir1:
2: pir2:
3: pir3:
4: pir4:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query				DB ID	Description
	Score	Match	Length	%		
1	58	46.4	691	1	TVWPAS	large T antigen -
2	58	46.4	695	1	TVWPTB	large T antigen -
3	57.5	46.0	688	1	TVWPTJ	large T antigen -
4	54.5	43.6	708	1	TVWPT4	large T antigen -
5	54	43.2	374	2	AG0937	hypothetical prote
6	53	42.4	435	2	D71857	hypothetical prote
7	53	42.4	435	2	B64658	hypothetical prote
8	51.5	41.2	894	2	T27007	hypothetical prote
9	51	40.8	519	2	E82932	spermidine/putresc
10	51	40.8	965	2	JQ0058	hypothetical l11K
11	50	40.0	455	2	T48973	cytochrome P450-11
12	50	40.0	2228	2	T14029	variant-specific s
13	49.5	39.6	1585	2	B69948	phage-related prot

14 49 39.2 200 2 T42547 gene 4 protein - e
15 49 39.2 629 2 T05089 hypothetical prote
16 48.5 38.8 188 2 A75382 hypothetical prote
17 48.5 38.8 217 2 S42877 ribosomal protein
18 48.5 38.8 218 2 JC4260 breast basic conse
19 48.5 38.8 331 2 A61046 ecdysone-induced m
20 48 38.4 45 2 C82233 hypothetical prote
21 48 38.4 115 2 AH1891 hypothetical prote
22 48 38.4 338 2 A82890 hypothetical prote
23 48 38.4 586 1 TVVPBP large T antigen -
24 48 38.4 652 2 T34497 hypothetical prote
25 48 38.4 935 2 T48778 hypothetical prote
26 47.5 38.0 200 2 AF2480 hypothetical prote
27 47.5 38.0 472 2 T41684 probable sterol o-
28 47.5 38.0 544 2 B84264 glycine betaine tr
29 47 37.6 121 2 T17708 hypothetical prote
30 47 37.6 371 2 T30292 glucosyl-transferr
31 47 37.6 371 2 AC0837 probable glycosylt
32 47 37.6 418 2 S40824 hypothetical 48K p
33 47 37.6 475 2 AI2439 hypothetical prote
34 47 37.6 497 2 T47715 hypothetical prote
35 47 37.6 710 2 T25734 hypothetical prote
36 47 37.6 753 2 A86756 prophage pi2 prote
37 47 37.6 823 2 T08092 plus fringe glycop
38 47 37.6 1103 2 T42022 probable chitin sy
39 47 37.6 1451 2 B86286 F9L1.15 protein -
40 47 37.6 1469 2 H96622 probable ABC trans
41 47 37.6 1711 2 C71625 variant-specific s
42 47 37.6 2182 2 T28634 variant-specific s
43 47 37.6 2197 2 B71600 variant-specific s
44 46.5 37.2 111 2 AH2530 hypothetical prote
45 46.5 37.2 315 2 F95855 probable oligopept

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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:39:39 ; Search time 7.70755 Seconds
(without alignments)
128.359 Million cell updates/sec

Title: US-09-915-914B-12
Perfect score: 125
Sequence: 1 KWEETWETWSQPKKKRV 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Search completed: March 1, 2004, 19:34:36

Job time : 13.5485 secs

SUMMARIES

Result No.	Query %			DB ID	Description
	Score	Match	Length		
1	58	46.4	691	1 TALA_POVBA	P14999 polycnaviru
2	58	46.4	695	1 TALA_POVBK	P03071 polycnaviru
3	57.5	46.0	688	1 TALA_POVJC	P03072 polycnaviru
4	54.5	43.6	708	1 TALA_SV40	P03070 simian viru
5	51	40.8	964	1 RRPO_MCW	P11640 maize chlor
6	49.5	39.6	508	1 MATK_LOTJA	Q9bbu2 lotus japon
7	49.5	39.6	1585	1 YQBO_BACSU	P45931 bacillus su
8	48.5	38.8	218	1 RL13_DROME	P41126 drosophila
9	48.5	38.8	504	1 MATK_NEPAL	Q95gt2 repenthes a
10	48.5	38.8	506	1 MATK_CALVU	Q47143 calluna vul
11	48.5	38.8	508	1 MATK_LOTPU	Q9tkp8 lotus pursh
12	48	38.4	41	1 LPW_VIBPA	P22100 vibrio para
13	48	38.4	176	1 CYT1_STOHE	P81662 stoichactis
14	48	38.4	586	1 TALA_POVBO	P24851 bovine poly
15	47.5	38.0	502	1 MATK_VACVI	Q8wi9 vaccinium v
16	47.5	38.0	503	1 MATK_VICSA	Q8mcj5 vicia sativ
17	47.5	38.0	503	1 MATK_VICVI	Q8mcj4 vicia villo

```

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OM protein - protein search, using sw model

Run on:      March 1, 2004, 16:40:39 ; Search time 35.5802 Seconds
              (without alignments)
              168.488 Million cell updates/sec

Title:       US-09-915-914B-12
Perfect score: 125
Sequence:    1 KMWETWETWSQPKKRRKV 19

Scoring table: BLOSUM62
              Gapop 10.0 , Gapext 0.5

Searched:    1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

```

```
Database :      SPREMBL_25:*
1:  sp_archaea:*
2:  sp_bacteria:*
3:  sp_fungi:*
4:  sp_human:*
5:  sp_invertebrate:*
6:  sp_mammal:*
7:  sp_mhc:*
8:  sp_organelle:*
9:  sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*
```

Result No.	Score	Query Match	Length	DB	ID	Description
---------------	-------	----------------	--------	----	----	-------------

1	63	50.4	793	17	Q8TVU1	Q8tvu1 methanopyru
2	57.5	46.0	688	12	Q91DF4	Q91df4 polyomaviru
3	57.5	46.0	688	12	Q8JUC5	Q8juc5 polyomaviru
4	57.5	46.0	688	12	Q8JUD5	Q8jud5 polyomaviru
5	57.5	46.0	688	12	Q9WM07	Q9wm07 polyomaviru
6	57.5	46.0	688	12	Q8V6G6	Q8v6g6 polyomaviru
7	57.5	46.0	688	12	Q8JWJ4	Q8jwj4 polyomaviru
8	57.5	46.0	688	12	Q9WM08	Q9wm08 polyomaviru
9	57.5	46.0	688	12	Q91DF8	Q91df8 polyomaviru
10	57.5	46.0	688	12	Q8JUD8	Q8jud8 polyomaviru
11	57.5	46.0	688	12	P88898	P88898 polyomaviru
12	57.5	46.0	688	12	Q8JUE2	Q8jue2 polyomaviru
13	57.5	46.0	688	12	Q91NL8	Q91nl8 polyomaviru
14	57.5	46.0	688	12	Q91DF5	Q91df5 polyomaviru
15	57.5	46.0	688	12	Q9W8D4	Q9w8d4 polyomaviru
16	57.5	46.0	688	12	Q91NM2	Q91nm2 polyomaviru
17	57.5	46.0	688	12	Q91NL2	Q91nl2 polyomaviru
18	57.5	46.0	688	12	Q8JZK0	Q8jzk0 polyomaviru
19	57.5	46.0	688	12	Q993Y4	Q993y4 polyomaviru
20	57.5	46.0	688	12	Q8V6G3	Q8v6g3 polyomaviru
21	57.5	46.0	688	12	Q9WM10	Q9wm10 polyomaviru
22	57.5	46.0	688	12	Q8JUC9	Q8juc9 polyomaviru
23	57.5	46.0	688	12	Q91DG7	Q91dg7 polyomaviru
24	57.5	46.0	688	12	Q91OD2	Q91od2 polyomaviru
25	57.5	46.0	688	12	Q8JZJ2	Q8jzj2 polyomaviru
26	57.5	46.0	688	12	Q8V6F7	Q8v6f7 polyomaviru
27	57.5	46.0	688	12	Q8JUB9	Q8jub9 polyomaviru
28	57.5	46.0	688	12	Q8JJK3	Q8jjk3 polyomaviru
29	57.5	46.0	688	12	Q9DPC9	Q9dpc9 polyomaviru
30	57.5	46.0	688	12	Q9DUG1	Q9dug1 polyomaviru
31	57.5	46.0	688	12	Q91DE6	Q91de6 polyomaviru
32	57.5	46.0	688	12	Q8JUB1	Q8jub1 polyomaviru
33	57.5	46.0	688	12	Q82950	Q82950 polyomaviru
34	57.5	46.0	688	12	Q8JUB6	Q8jub6 polyomaviru
35	57.5	46.0	688	12	Q8V6H1	Q8v6h1 polyomaviru
36	57.5	46.0	688	12	Q91NL5	Q91nl5 polyomaviru
37	57.5	46.0	688	12	Q8V6G7	Q8v6g7 polyomaviru
38	57.5	46.0	688	12	Q9DUG4	Q9dug4 polyomaviru
39	57.5	46.0	688	12	Q8JWJ3	Q8jwj3 polyomaviru
40	57.5	46.0	688	12	Q91DH4	Q91dh4 polyomaviru
41	57.5	46.0	688	12	Q8JWI7	Q8jwi7 polyomaviru
42	57.5	46.0	688	12	Q8JUC2	Q8juc2 polyomaviru
43	57.5	46.0	688	12	Q993Y5	Q993y5 polyomaviru
44	57.5	46.0	688	12	Q8JUE1	Q8jue1 polyomaviru
45	57.5	46.0	688	12	Q91DH0	Q91dh0 polyomaviru

Search completed: March 1, 2004, 19:32:06
Job time : 36.5802 secs

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OM protein - protein search, using sw model

Run on: March 1, 2004, 13:31:13 ; Search time 55.6698 Seconds
(without alignments)
106.584 Million cell updates/sec

Title: US-09-915-914B-1
Perfect score: 134
Sequence: 1 YGFKRRWSQPKETWETWTE 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues
Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Listing first 45 summaries

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Match	Length DB	ID	Description
1	134	100.0	21	5	ABB77665
2	79.5	59.3	18	5	ABB77666
3	79	59.0	17	5	ABB77667
4	77.5	57.8	25	5	ABB78714
5	77	57.5	20	5	ABB77679
6	75	56.0	19	5	ABB77668
7	75	56.0	19	5	ABB77698
8	75	56.0	19	5	ABB77669
9	74	55.2	1185	5	AAU80135

10	* 74	55.2	1185	6	AAE33407
11	68	50.7	10	5	ABB78711
12	68	50.7	21	5	ABB78716
13	68	50.7	430	5	ABP47755
14	68	50.7	560	4	AAB84201
15	68	50.7	560	6	AAG79973
16	68	50.7	560	7	ADE29023
17	68	50.7	562	6	ABR44741
18	68	50.7	562	6	ABR44740
19	68	50.7	565	6	ABR44743
20	68	50.7	724	5	AAU11869
21	68	50.7	739	5	AAU11874
22	68	50.7	760	1	AAP94510
23	68	50.7	850	4	AAE04792
24	68	50.7	850	4	AAE04791
25	68	50.7	850	5	ADE71141
26	68	50.7	850	5	ADE71143
27	68	50.7	850	6	ABU63365
28	68	50.7	850	6	ABU63366
29	68	50.7	875	4	AAE04794
30	68	50.7	875	4	AAE04793
31	68	50.7	875	5	ADE71145
32	68	50.7	875	5	ADE71147
33	68	50.7	875	6	ABU63368
34	68	50.7	875	6	ABU63367
35	68	50.7	902	3	AAB12995
36	68	50.7	912	2	AAR08053
37	68	50.7	912	2	AAR08057
38	68	50.7	979	4	AAG80980
39	68	50.7	1002	3	AAB69281
40	68	50.7	1003	1	AAP60420
41	68	50.7	1003	1	AAP70861
42	68	50.7	1003	5	AAO19387
43	68	50.7	1003	6	AAO30963
44	68	50.7	1010	2	AAR91823
45	68	50.7	1012	1	AAP61507

ALIGNMENTS

RESULT 1
ABB77665
ID ABB77665 standard; peptide; 21 AA.
XX ABB77665;
AC ABB77665;
XX 01-JUL-2002 (first entry)
XX Peptide transfection agent Pep-1.
DE Peptide transfection agent Pep-1.
XX
KW Intracellular delivery; transfection agent; cancer; infectious disease; peptide vector.
KW
XX
OS Synthetic.
XX
PN W0200210201-A2.

```

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OM protein - protein search, using sw model

Run on:      March 1, 2004, 16:46:26 ; Search time 13.7689 Seconds
              (without alignments)
              146.709 Million cell updates/sec

Title:       US-09-915-914B-1
Perfect score: 134
Sequence:    1 YGFKRRWSQPKETWETWTE 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:    283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :    PIR 78:*
              1: pir1:*
              2: pir2:*
              3: pir3:*
              4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result      %
No.  Score  Match Length DB  ID  Description
-----
1    70    52.2  559  2  B47175  reverse transcript
2    68    50.7  1003  1  GNVWL  HIV-1 retropepsin
3    68    50.7  1003  1  B44001  HIV-1 retropepsin
4    68    50.7  1003  2  T09440  pol polyprotein -
5    68    50.7  1012  1  GNVWL  HIV-1 retropepsin
6    68    50.7  1015  1  GNVWH3  HIV-1 retropepsin
7    63    47.0  902  2  T01668  pol polyprotein -
8    63    47.0  1002  2  S54378  pol polyprotein -
9    62    46.3  1002  1  GNLJND  HIV-1 retropepsin
10   60    44.8  487  4  S51886  hypothetical prote
11   60    44.8  492  2  S51885  probable membrane
12   60    44.8  528  4  S51887  hypothetical prote

```

14 57 42.5 559 2 A47175 reverse transcript
15 57 42.5 912 2 S33980 pol polyprotein -
16 57 42.5 1003 1 GNVWA2 HIV-1 retropepsin
17 55 41.0 69 2 JQ1257 hypothetical 7.6K
18 55 41.0 1027 1 GNLJ51 HIV-1 retropepsin
19 53 39.6 1058 2 S08436 pol polyprotein -
20 52 38.8 1056 1 GNLJG3 HIV-1 retropepsin
21 51 38.1 376 2 H82988 hypothetical prote
22 50.5 37.7 150 2 S36991 transposase (clone
23 50 37.3 392 2 T19698 hypothetical prote
24 50 37.3 426 2 T14527 S-locus-specific g
25 50 37.3 509 2 T51806 cytochrome P450 ka
26 50 37.3 669 2 T13335 hypothetical prote
27 50 37.3 1019 2 T11560 pol polyprotein -
28 49.5 36.9 860 2 JC5986 A-kinase anchoring
29 49.5 36.9 1451 2 B86286 F9Li.15 protein -
30 49.5 36.9 1469 2 H96622 probable ABC trans
31 49 36.6 201 2 T49792 hypothetical prote
32 49 36.6 214 2 AC2726 DNA-binding protei
33 49 36.6 229 2 G97507 probable DNA-bindi
34 49 36.6 234 2 B58934 subunit of ABC tra
35 49 36.6 303 2 AE3201 conserved hypothet
36 49 36.6 472 1 WMADF6 early E1B 52K prot
37 49 36.6 535 2 T41384 hypothetical prote
38 49 36.6 633 2 S60408 probable membrane
39 49 36.6 669 2 T13640 probable minor str
40 49 36.6 670 2 T09274 hypothetical prote
41 49 36.6 670 2 T09205 hypothetical prote
42 49 36.6 1035 1 GNLJGG HIV-1 retropepsin
43 49 36.6 1510 2 C84727 probable glucan sy
44 49 36.6 1878 2 E86189 hypothetical prote
45 48.5 36.2 727 2 T47541 beta-galactosidase

Search completed: March 1, 2004, 19:34:20
Job time : 16.8598 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:46:26 ; Search time 13.7689 Seconds
(without alignments)
146.709 Million cell updates/sec

Title: US-09-915-914B-1
Perfect score: 134
Sequence: 1 YGFKRRWSQPKETWETWTE 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: Pir1:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	70	52.2	559	2	B47175	reverse transcript
2	68	50.7	1003	1	GNWLV	HIV-1 retropepsin
3	68	50.7	1003	1	B44001	HIV-1 retropepsin
4	68	50.7	1003	2	T09440	pol polyprotein -
5	68	50.7	1012	1	GNWVL	HIV-1 retropepsin
6	68	50.7	1015	1	GNWH3	HIV-1 retropepsin
7	63	47.0	902	2	T01668	pol polyprotein -
8	63	47.0	1002	2	S54378	pol polyprotein -
9	62	46.3	1002	1	GNLJND	HIV-1 retropepsin
10	60	44.8	487	4	S51886	hypothetical prote
11	60	44.8	492	2	S51885	probable membrane
12	60	44.8	528	4	S51887	hypothetical prote
13	59	44.0	420	2	D69769	cellulose synthase

14 reverse transcript
15 pol polyprotein -
16 HIV-1 retropepsin
17 hypothetical 7.6K
18 HIV-1 retropepsin
19 pol polyprotein -
20 HIV-1 retropepsin
21 hypothetical prote
22 transposase (clone
23 hypothetical prote
24 S-locus-specific g
25 cytochrome P450 ka
26 pol polyprotein -
27 A-kinase anchoring
28 F9L1.15 protein -
29 probable ABC trans
30 hypothetical prote
31 DNA-binding protei
32 probable DNA-bind
33 subunit of ABC tra
34 conserved hypothet
35 early E1B 52K prot
36 hypothetical prote
37 probable membrane
38 probable minor str
39 hypothetical prote
40 hypothetical prote
41 HIV-1 retropepsin
42 probable glucan sy
43 hypothetical prote
44 beta-galactosidase
45

57 42.5 559 2 A47175
57 42.5 912 2 S33980
57 42.5 1003 1 GNWAZ
55 41.0 69 2 JQ1257
55 41.0 1027 1 GNLJ51
53 39.6 1058 2 S08436
52 38.8 1056 1 GNLJG3
51 38.1 376 2 H82988
50.5 37.7 150 2 S36991
50 37.3 392 2 T19698
50 37.3 426 2 T14527
50 37.3 509 2 T51806
50 37.3 669 2 T13335
50 37.3 1019 2 T11560
49.5 36.9 860 2 JC5986
49.5 36.9 1451 2 B86286
49.5 36.9 1469 2 H96622
49 36.6 201 2 T49792
49 36.6 214 2 AC2726
49 36.6 229 2 G97507
49 36.6 234 2 B58934
49 36.6 303 2 AE3201
49 36.6 472 1 WMADP6
49 36.6 535 2 T41384
49 36.6 633 2 S60408
49 36.6 669 2 T13640
49 36.6 670 2 T09274
49 36.6 670 2 T09205
49 36.6 1035 1 GNLJGG
49 36.6 1510 2 C84727
49 36.6 1878 2 E86189
48.5 36.2 727 2 T47541

Search completed: March 1, 2004, 19:34:20
Job time : 16.8598 secs

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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:40:39 ; Search time 39.3255 Seconds
(without alignments)
168.488 Million cell updates/sec

Title: US-09-915-914B-1
Perfect score: 134
Sequence: 1 YGFKRRWSQPKEWTETWTE 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archheap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	
No.	Score	Match Length DB ID Description

1 73 54.5 1433 15 Q8AE23 human immun
2 70 52.2 559 15 Q9PXX1 human immun
3 69 51.5 237 15 Q9WGW1 human immun
4 69 51.5 562 15 Q99AZ9 human immun
5 69 51.5 591 15 Q8Q884 human immun
6 69 51.5 1003 15 Q8AC79 human immun
7 68 50.7 212 15 Q9WGU7 human immun
8 68 50.7 225 15 Q998V3 human immun
9 68 50.7 237 15 Q9WGV0 human immun
10 68 50.7 237 15 Q9WGV3 human immun
11 68 50.7 237 15 Q9WGV7 human immun
12 68 50.7 237 15 Q9WGW5 human immun
13 68 50.7 237 15 Q9WGW0 human immun
14 68 50.7 237 15 Q9WGV5 human immun
15 68 50.7 237 15 Q9WGV9 human immun
16 68 50.7 237 15 Q9W8H5 human immun
17 68 50.7 237 15 Q9W9U0 human immun
18 68 50.7 237 15 Q9WGX6 human immun
19 68 50.7 237 15 Q9WGW2 human immun
20 68 50.7 237 15 Q9WGX5 human immun
21 68 50.7 237 15 Q9WGV2 human immun
22 68 50.7 237 15 Q9WGU8 human immun
23 68 50.7 237 15 Q9WGW6 human immun
24 68 50.7 237 15 Q9WGV6 human immun
25 68 50.7 237 15 Q9WGV8 human immun
26 68 50.7 237 15 Q9WGW3 human immun
27 68 50.7 237 15 Q9WGW4 human immun
28 68 50.7 237 15 Q9WGV1 human immun
29 68 50.7 237 15 Q9WGV4 human immun
30 68 50.7 433 15 Q79787 human immun
31 68 50.7 514 15 Q9DLJ8 human immun
32 68 50.7 519 15 Q9IDI3 human immun
33 68 50.7 523 15 Q9IDI9 human immun
34 68 50.7 523 15 Q9IDC7 human immun
35 68 50.7 523 15 Q9IDB6 human immun
36 68 50.7 523 15 Q9IDB2 human immun
37 68 50.7 523 15 Q9IDF2 human immun
38 68 50.7 523 15 Q9IDB0 human immun
39 68 50.7 524 15 Q9IDJ7 human immun
40 68 50.7 524 15 Q9IDI8 human immun
41 68 50.7 524 15 Q9IDI7 human immun
42 68 50.7 524 15 Q9IDD1 human immun
43 68 50.7 524 15 Q9IDI6 human immun
44 68 50.7 524 15 Q9IDB8 human immun
45 68 50.7 524 15 Q9IDI2 human immun

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OM protein - protein search, using sw model

Run on: March 1, 2004, 13:31:13 ; Search time 47.717 Seconds
(without alignments)
106.584 Million cell updates/sec

Title: US-09-915-914B-2
Perfect score: 120
Sequence: 1 YGFKKRRQPTWETWTE 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query			Description	
No.	Score	Match	Length	DB ID		
1	120	100.0	18	5	ABB77666	Abb77666 Peptide t
2	102.5	85.4	17	5	ABB77667	Abb77667 Peptide t
3	99.5	82.9	20	5	ABB77679	Abb77679 Generic p
4	97.5	81.2	19	5	ABB77668	Abb77668 Peptide t
5	97.5	81.2	19	5	ABB77698	Abb77698 Peptide t
6	97.5	81.2	19	5	ABB77669	Abb77669 Peptide t
7	79.5	66.2	21	5	ABB77665	Abb77665 Peptide t
8	69	57.5	9	5	ABB77692	Abb77692 Peptide t
9	69	57.5	11	5	ABB77695	Abb77695 Peptide t

Search completed: March 1, 2004, 19:31:49
Job time : 44.3255 secs

10 69 57.5 12 5 ABB77689 Abb77689 Hydrophob
11 69 57.5 12 5 ABP56174 Abp56174 Cell-targ
12 69 57.5 20 5 ABB77672 Abb77672 Peptide t
13 69 57.5 20 5 ABB77673 Abb77673 Peptide t
14 69 57.5 21 5 ABG78995 Abg78995 Cell pene
15 69 57.5 21 5 ABB77693 Abb77693 Peptide t
16 69 57.5 21 5 ABB77671 Abb77671 Peptide t
17 69 57.5 21 7 ADB68484 Adb68484 Peptide s
18 69 57.5 21 7 ADC22460 Adc22460 Protein-d
19 69 57.5 26 5 ABP56200 Abp56200 Chimeric
20 64.5 53.8 19 5 ABB77670 Abb77670 Peptide t
21 59 49.2 19 5 ABB10106 Abb10106 Peptide t
22 59 49.2 19 5 ABB77699 Abb77699 Peptide t
23 59 49.2 20 5 ABB77694 Abb77694 Peptide t
24 59 49.2 21 5 ABB77674 Abb77674 Peptide t
25 58 48.3 430 5 ABP47755 Abp47755 Protein #
26 58 48.3 560 4 AAB84201 Aab84201 Amino aci
27 58 48.3 560 6 AAG79973 Aag79973 P2C/C38S/
28 58 48.3 560 7 ADE29023 Ade29023 HIV-1 RT_
29 58 48.3 562 6 ABR44741 Abr44741 Plasmid p
30 58 48.3 562 6 ABR44740 Abr44740 Plasmid p
31 58 48.3 565 6 ABR44743 Abr44743 Plasmid 7
32 58 48.3 724 5 AAU11869 Aau11869 HIV pol p
33 58 48.3 739 5 AAU11874 Aau11874 HIV pol p
34 58 48.3 760 1 AAP94510 Aap94510 Sequence
35 58 48.3 850 4 AAE04792 Aae04792 Human imm
36 58 48.3 850 4 AAE04791 Aae04791 Human imm
37 58 48.3 850 5 ADE71141 Ade71141 Codon opt
38 58 48.3 850 5 ADE71143 Ade71143 Inactivat
39 58 48.3 850 6 ABU63365 Abu63365 HIV-1 wil
40 58 48.3 850 6 ABU63366 Abu63366 HIV-1 ina
41 58 48.3 875 4 AAE04794 Aae04794 Human tPA
42 58 48.3 875 4 AAE04793 Aae04793 Human tPA
43 58 48.3 875 5 ADE71145 Ade71145 Codon opt
44 58 48.3 875 5 ADE71147 Ade71147 Inactivat
45 58 48.3 875 6 ABU63368 Abu63368 HIV-1 ina

ALIGNMENTS

RESULT 1
ABB77666
ID ABB77666 standard; peptide; 18 AA.
XX
AC ABB77666;
XX
DT 01-JUL-2002 (first entry)
XX
DE Peptide transfection agent Pep-1.1.
XX
KW Intracellular delivery; transfection agent; cancer; infectious disease;
KW peptide vector.
XX
OS Synthetic.
XX
PN W0200210201-A2.

XX 07-FEB-2002.
PD
XX
PF 26-JUL-2001; 2001WO-US023406.
XX
PR 31-JUL-2000; 2000US-0221932P.
XX
PA (ACTI-) ACTIVE MOTIF.
PA (CNRS) CENT NAT RECH SCI.
XX
PI Divida G, Morris M, Mery J, Heitz F, Fernandez J, Archdeacon J;
PI Horndorp K;
XX
DR WPI; 2002-329441/36.
XX
XX
PT Transfection agent that comprises a peptide comprising hydrophobic and
PT hydrophilic domain and having amino acid residues of specified length is
PT useful for a non-covalent association with and transport of a
PT heterologous compound into a cell.
XX
PS Claim 12; Page 16; 156pp; English.
XX
CC The invention relates to a transfection agent comprises a peptide of
CC about 16 - 30 amino acids in length. Peptides of the invention comprise a
CC hydrophobic domain, a hydrophilic domain, optionally a spacer sequence
CC between the domains and a functional group conjugated to at least one
CC terminal of the peptide. Peptides of the invention are useful for a non-
CC covalent association with and transport of a heterologous compound into a
CC cell. They are also useful for promoting the cellular internalisation of
CC at least one member e.g. peptide, proteins, antibodies, their derivatives
CC and/or conjugates. They may form part of a pharmaceutical composition to
CC deliver the compound selected from a diagnostic or therapeutic compound,
CC to treat at least one condition such as cancer or an infectious disease,
CC or which targets a cancerous cell or pathogen-infected cell and to
CC deliver a peptide or inhibitor that disrupts the activity of the enzyme.
CC The agent of the invention has a transfection efficiency of at least 5%
CC for at least two of the members of the group of the compounds. The agent
CC has a good delivery efficiency for a broad spectrum of compounds and cell
CC types, has a low toxicity, are easy to handle and easy to formulate in
CC conjunction with the many different compound types that it can deliver.
CC The peptides are serum sensitive, thus they bode particularly well for
CC systemic and/or localised in patients. The current sequence represents
CC the peptide transfection agent Pep-1.1
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 120; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGFKRRRQPTWWETWTE 18
| | | | | | | | | | | | | | | |
Db 1 YGFKRRRQPTWWETWTE 18

Search completed: March 1, 2004, 16:55:39
Job time : 48.717 secs

OM protein - protein search, using sw model

Run on: March 1, 2004, 16:46:26 ; Search time 11.8019 Seconds
(without alignments)
146.709 Million cell updates/sec

Title: US-09-915-914B-2
Perfect score: 120
Sequence: 1 YGFKRRRQPTWETWTE 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	58	48.3	559	2	B47175	reverse transcript
2	58	48.3	1003	1	GNVWL	HIV-1 retropepsin
3	58	48.3	1003	1	B44001	HIV-1 retropepsin
4	58	48.3	1003	2	T09440	pol polyprotein -
5	58	48.3	1012	1	GNVWL	HIV-1 retropepsin
6	58	48.3	1015	1	GNVWH3	HIV-1 retropepsin
7	54	45.0	276	2	T29689	hypothetical prote
8	52	43.3	1002	1	GNLJND	HIV-1 retropepsin
9	51	42.5	413	2	C91229	hypothetical prote
10	51	42.5	413	2	B86076	hypothetical prote
11	51	42.5	418	2	S40824	hypothetical 48K p
12	51	42.5	424	2	T05785	hypothetical prote
13	50	41.7	567	2	E96764	ethylene-insensiti

14	50	41.7	902	2	T01668	pol polyprotein -
15	50	41.7	1002	2	S54378	pol polyprotein -
16	49	40.8	309	1	B64041	hypothetical prote
17	47.5	39.6	239	2	C84505	hypothetical prote
18	47	39.2	226	2	T20645	hypothetical prote
19	47	39.2	559	2	A47175	reverse transcript
20	47	39.2	747	2	AG3031	conserved hypothet
21	47	39.2	747	2	D98254	hypothetical prote
22	47	39.2	912	2	S33980	pol polyprotein -
23	47	39.2	1003	1	GNVWA2	HIV-1 retropepsin
24	46.5	38.8	333	2	H82852	hydroxybenzoate oc
25	46.5	38.8	688	1	IVVPTJ	large r antigen -
26	46	38.3	392	2	D82330	conserved hypothet
27	46	38.3	456	2	A71501	probable hexosphos
28	46	38.3	456	2	G81660	Glpt/Pgpt/Uhpt fam
29	46	38.3	471	2	T50016	transcription fact
30	46	38.3	512	2	S41881	alpha-amylase (EC
31	46	38.3	823	2	T08092	plus fringe glycop
32	45	37.5	130	2	A82599	conserved hypothet
33	45	37.5	144	2	Ai3330	hypothetical prote
34	45	37.5	334	2	T49195	hypothetical prote
35	45	37.5	455	2	F86573	hexcosphate tra
36	45	37.5	455	2	A72050	Glpt/Pgpt/Uhpt fam
37	45	37.5	584	2	B84668	ethylene-insensiti
38	45	37.5	627	2	E95377	probable two-compo
39	45	37.5	1009	2	S28081	pol polyprotein -
40	45	37.5	2478	2	AH2140	polyketide synthas
41	44.5	37.1	385	2	A47245	acyl-facyl-carrier
42	44.5	37.1	633	2	S60408	probable membrane
43	44	36.7	121	2	A71031	hypothetical prote
44	44	36.7	401	2	T32167	hypothetical prote
45	44	36.7	535	2	AE2710	MFS permease [impo

Search completed: March 1, 2004, 19:34:24
Job time : 15.8928 secs

OM protein - protein search, using sw model
Run on: March 1, 2004, 16:39:39 ; Search time 7.30189 Seconds
(without alignments)
128.359 Million cell updates/sec

Title: US-09-915-914B-2
Perfect score: 120
Sequence: 1 YGFKRRRQPTWETWTE 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query				Description
	Score	Match	Length	DB ID	
1	58	48.3	1003	1	POL_HV1H2
2	58	48.3	1003	1	POL_HV1Y2
3	58	48.3	1007	1	POL_HV1JR
4	58	48.3	1015	1	POL_HV1B1
5	58	48.3	1015	1	POL_HV1B5
6	58	48.3	1015	1	POL_HV1BR
7	58	48.3	1015	1	POL_HV1PV
8	55	45.8	1006	1	POL_HV1MN
9	53	44.2	1002	1	POL_HV1RH
10	53	44.2	1003	1	POL_HV1N5
11	53	44.2	1003	1	POL_HV1OY
12	52	43.3	1002	1	POL_HV1ND
13	51	42.5	68	1	ATP8_HIPAM
14	51	42.5	413	1	YIHS_ECOLI
15	50	41.7	567	1	EIL3_ARATH
16	50	41.7	1002	1	POL_HV1EL
17	50	41.7	1002	1	POL_HV1MA
					P04585 human immu
					P35963 human immu
					P20875 human immu
					P03366 human immu
					P04587 human immu
					P03367 human immu
					P03368 human immu
					P05961 human immu
					P05959 human immu
					P12497 human immu
					P20892 human immu
					P18802 human immu
					Q9zzy7 hippopotamu
					P32140 escherichia
					O23116 arabadopsis
					P04589 human immu
					P04588 human immu

18	50	41.7	1002	1	POL_HV1Z2
19	49	40.8	309	1	YBGK_HAEIN
20	47	39.2	66	1	ATP8_CEREH
21	47	39.2	557	1	EIL5_ARATH
22	47	39.2	1003	1	POL_HV1A2
23	46.5	38.8	278	1	RCEL_CHRVI
24	46.5	38.8	688	1	TALA_POVJC
25	46	38.3	78	1	YO09_BPL2
26	46	38.3	456	1	UHPT_CHLMU
27	46	38.3	456	1	UHPT_CHLTR
28	46	38.3	471	1	EIL4_ARATH
29	45	37.5	149	1	RS19_METKA
30	45	37.5	455	1	UHPT_CHLPN
31	45	37.5	584	1	EILI_ARATH
32	45	37.5	1009	1	POL_SIVGB
33	44.5	37.1	276	1	RCEL_RHOPA
34	44.5	37.1	385	1	STAD_CORSA
35	44.5	37.1	633	1	GYP3_YEAST
36	44	36.7	119	1	YF56_PYREFU
37	44	36.7	121	1	YF39_PYRHO
38	44	36.7	470	1	PROP_CAVPO
39	44	36.7	518	1	EIL2_ARATH
40	44	36.7	628	1	EIN3_ARATH
41	44	36.7	1002	1	POL_HV1U4
42	44	36.7	1019	1	POL_SIVS4
43	44	36.7	1022	1	POL_SIVSP
44	44	36.7	1027	1	POL_SIVCZ
45	44	36.7	1039	1	M2C1_MOUSE
					P12499 human immu
					P44298 haemophilus
					Q9mqj9 cervus elap
					Q9fjq5 arabadopsis
					P03369 human immu
					P51762 chromatium
					P03072 polyomaviru
					P42544 bacterioph
					Q9pj8 chlamydia m
					O84548 chlamydia t
					Q9lxl6 arabadopsis
					Q8twp2 methanopyru
					Q9z7n9 chlamydia p
					Q9slh0 arabadopsis
					P22382 simian immu
					O83005 rhodopsendo
					P32063 coriandrum
					P48566 saccharomyc
					Q8u0n0 pyrococcus
					O74017 pyrococcus
					Q64181 cavia porce
					O23115 arabadopsis
					O24606 arabadopsis
					P24740 human immu
					P12502 simian immu
					P19505 simian immu
					P17283 chimpanzee
					Q91w89 mus musculu

Search completed: March 1, 2004, 19:24:59
Job time : 9.30189 secs

OM protein - protein search, using sw model

Run on: March 1, 2004, 16:40:39 ; Search time 33.7076 Seconds
(without alignments)
168.488 Million cell updates/sec

Title: US-09-915-914B-2
Perfect score: 120
Sequence: 1 YGFKRRRQPTWETWTE 18
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*

1:	sp_archaea:*
2:	sp_bacteria:*
3:	sp_fungi:*
4:	sp_human:*
5:	sp_invertebrate:*
6:	sp_mammal:*
7:	sp_mhc:*
8:	sp_organelle:*
9:	sp_phage:*
10:	sp_plant:*
11:	sp_rodent:*
12:	sp_virus:*
13:	sp_vertebrate:*
14:	sp_unclassified:*
15:	sp_rvirus:*
16:	sp_bacteriap:*
17:	sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description

1	60	50.0	561	15	Q9DIJ0	Q9di10 human immun
2	58	48.3	212	15	Q9WGU7	Q9wgu7 human immun
3	58	48.3	237	15	Q9WGV0	Q9wgv0 human immun
4	58	48.3	237	15	Q9WGU0	Q9w9u0 human immun
5	58	48.3	237	15	Q9WGV2	Q9wgv2 human immun
6	58	48.3	237	15	Q9WGU8	Q9wgu8 human immun
7	58	48.3	237	15	Q9WGV1	Q9wgv1 human immun
8	58	48.3	433	15	Q79787	Q79787 human immun
9	58	48.3	523	15	Q9IDB6	Q9idb6 human immun
10	58	48.3	523	15	Q9IDB2	Q9idb2 human immun
11	58	48.3	523	15	Q9IDB0	Q9idb0 human immun
12	58	48.3	524	15	Q9IDB8	Q9idb8 human immun
13	58	48.3	545	15	Q90S14	Q90s14 human immun
14	58	48.3	546	15	Q90S15	Q90s15 human immun
15	58	48.3	547	15	Q90S83	Q90s83 human immun
16	58	48.3	547	15	Q90S82	Q90s82 human immun
17	58	48.3	559	15	Q8UTV9	Q8utv9 human immun
18	58	48.3	559	15	Q9PXX1	Q9pxx1 human immun
19	58	48.3	560	15	Q99BA2	Q99ba2 human immun
20	58	48.3	560	15	Q99BA1	Q99ba1 human immun
21	58	48.3	560	15	Q99BA4	Q99ba4 human immun
22	58	48.3	560	15	Q90RP3	Q90rp3 human immun
23	58	48.3	560	15	Q90EW4	Q90ew4 human immun
24	58	48.3	560	15	Q90RN6	Q90rn6 human immun
25	58	48.3	560	15	Q90RN3	Q90rn3 human immun
26	58	48.3	560	15	Q90EV9	Q90ev9 human immun
27	58	48.3	560	15	Q99BA3	Q99ba3 human immun
28	58	48.3	560	15	Q90EW1	Q90ew1 human immun
29	58	48.3	560	15	Q99BA5	Q99ba5 human immun
30	58	48.3	560	15	Q90RN4	Q90rn4 human immun
31	58	48.3	560	15	Q90RP4	Q90rp4 human immun
32	58	48.3	560	15	Q90RR8	Q90rr8 human immun
33	58	48.3	560	15	Q90RN5	Q90rn5 human immun
34	58	48.3	560	15	Q90RQ5	Q90rq5 human immun
35	58	48.3	560	15	Q90RP2	Q90rp2 human immun
36	58	48.3	560	15	Q90RR9	Q90rr9 human immun
37	58	48.3	560	15	Q99B99	Q99b99 human immun
38	58	48.3	560	15	Q90EW2	Q90ew2 human immun
39	58	48.3	560	15	Q99BA7	Q99ba7 human immun
40	58	48.3	560	15	Q90RR7	Q90rr7 human immun
41	58	48.3	560	15	Q71153	Q71153 human immun
42	58	48.3	560	15	Q90EW7	Q90ew7 human immun
43	58	48.3	560	15	Q90RQ6	Q90rq6 human immun
44	58	48.3	560	15	Q75395	Q75395 human immun
45	58	48.3	560	15	Q90RP5	Q90rp5 human immun

Search completed: March 1, 2004, 19:31:50
Job time : 34.7076 secs

OM protein - protein search, using sw model

Run on: March 1, 2004, 13:31:13 ; Search time 45.066 Seconds
(without alignments)
106.584 Million cell updates/sec

Title: US-09-915-914B-3
Perfect score: 113
Sequence: 1 YGPKRRQTWETWTE 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	113	100.0	17	5	ABB77667
2	102.5	90.7	18	5	ABB77666
3	92	81.4	20	5	ABB77679
4	90	79.6	19	5	ABB77668
5	90	79.6	19	5	ABB77698
6	90	79.6	19	5	ABB77669
7	79	69.9	21	5	ABB77665
8	73	64.6	11	5	ABB77695
9	73	64.6	12	5	ABB77689

10	73	64.6	12	5	ABP56174	Abp56174	Cell-targ
11	73	64.6	20	5	ABB77672	Abb77672	Peptide t
12	73	64.6	20	5	ABB77673	Abb77673	Peptide t
13	73	64.6	21	5	ABG78995	Abg78995	Cell pene
14	73	64.6	21	5	ABB77693	Abb77693	Peptide t
15	73	64.6	21	5	ABB77671	Abb77671	Peptide t
16	73	64.6	21	7	ADB68484	Adb68484	Peptide s
17	73	64.6	21	7	ADC22460	Adc22460	Protein-d
18	73	64.6	26	5	ABP56200	Abp56200	Chimeric
19	69	61.1	9	5	ABB77692	Abb77692	Peptide t
20	66.5	58.8	19	5	ABB77670	Abb77670	Peptide t
21	63	55.8	20	5	ABB77694	Abb77694	Peptide t
22	63	55.8	21	5	ABB77674	Abb77674	Peptide t
23	60	53.1	19	5	ABB10106	Abb10106	Peptide t
24	60	53.1	19	5	ABB77699	Abb77699	Peptide t
25	57	50.4	21	5	ABB78716	Abb78716	Peptide p
26	55.5	49.1	19	5	ABB77675	Abb77675	Peptide t
27	55	48.7	21	5	ABB77678	Abb77678	Generic p
28	54	47.8	19	5	ABB77676	Abb77676	Peptide t
29	53.5	47.3	25	5	ABB78714	Abb78714	Retroinhi
30	53	46.9	9	4	ABP23078	Abp23078	HIV A11 m
31	53	46.9	9	4	ABP19745	Abp19745	HIV A01 m
32	53	46.9	9	4	ABP11817	Abp11817	HIV A01 s
33	53	46.9	9	4	ABP16014	Abp16014	HIV A24 s
34	53	46.9	9	4	ABP16168	Abp16168	HIV A24 s
35	53	46.9	9	4	ABP21039	Abp21039	HIV A03 m
36	53	46.9	9	4	ABP19747	Abp19747	HIV A01 m
37	53	46.9	10	4	ABP18045	Abp18045	HIV B58 s
38	53	46.9	10	5	ABB78711	Abb78711	HIV-1 BH1
39	53	46.9	430	5	ABP47755	Abp47755	Protein #
40	53	46.9	560	4	AAB84201	Aab84201	Amino aci
41	53	46.9	560	6	AAG79973	Ag79973	P2C/C38S/
42	53	46.9	560	7	ADE29023	Ade29023	HIV-1 RT-
43	53	46.9	562	6	ABR44741	Abr44741	Plasmid p
44	53	46.9	562	6	ABR44740	Abr44740	Plasmid p
45	53	46.9	565	6	ABR44743	Abr44743	Plasmid 7

ALIGNMENTS

RESULT 1
ABB77667

ID ABB77667 standard; peptide; 17 AA.

XX ABB77667;

AC ABB77667;

XX 01-JUL-2002 (first entry)

DT 01-JUL-2002 (first entry)

XX Peptide transfection agent Pep-1.2.

DE Peptide transfection agent Pep-1.2.

XX Intracellular delivery; transfection agent; cancer; infectious disease;

KW peptide vector.

XX Synthetic.

OS Synthetic.

XX WO200210201-A2.

PN WO200210201-A2.

14 hypothetical prote
15 env polypept
16 hypothetical prote
17 hexosphosphate tra
18 GlpT/Pgpr/Uhpt fam
19 probable hexosphos
20 GlpT/Pgpr/Uhpt fam
21 pol polypept
22 pol polypept
23 chloroplast envelo
24 hypothetical prote
25 probable membrane
26 HIV-1 retropepsin
27 hypothetical prote
28 hypothetical prote
29 plus fringe glycop
30 probable chitin sy
31 KIAA0637 protei
32 hypothetical prote
33 conserved hypothet
34 hypothetical prote
35 hypothetical prote
36 hypothetical prote
37 related to RCC1 pr
38 hypothetical prote
39 hypothetical prote
40 erythrocyte membra
41 hypothetical prote
42 hypothetical prote
43 hypothetical prote
44 6-HYDROXY-D-NICOTI
45

49 43.4
48.5 42.9
48 42.5
48 42.5
48 42.5
48 42.5
48 42.5
48 42.5
48 42.5
47 41.6
47 41.6
47 41.6
46.5 41.2
46 40.7
46 40.7
46 40.7
46 40.7
45.5 40.3
45 39.8
45 39.8
45 39.8
45 39.8
45 39.8
45 39.8
45 39.8
45 39.8
44.5 39.4
44.5 39.4
44.5 39.4

528 4 S51887
859 1 VCLJE3
268 2 B87676
455 2 F86573
455 2 A72050
456 2 A71501
456 2 G81660
902 2 T01668
1002 2 S54378
229 2 T06346
431 2 AH2006
633 2 S60408
1002 1 GNLJND
1768 2 E85062
269 2 F95946
502 2 T41541
823 2 T08092
1103 2 T42022
1171 2 T00380
836 2 T31613
130 2 A82599
238 2 S73123
298 2 B71872
334 2 T49195
531 2 T50964
621 2 H84922
689 2 T35882
2212 2 T28157
2647 2 T28161
121 2 A71031
239 2 C84505
511 2 T48777

Search completed: March 1, 2004, 19:34:25
Job time : 12.2371 secs

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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:39:39 ; Search time 6.89623 Seconds
(without alignments)
128.359 Million cell updates/sec

Title: US-09-915-914B-3
Perfect score: 113
Sequence: 1 YGFKRRQTWETWTE 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	53	46.9	1003	1	POL_HV1H2 P04585 human immun
2	53	46.9	1003	1	POL_HV1Y2 P35963 human immun
3	53	46.9	1006	1	POL_HV1MN P05961 human immun
4	53	46.9	1007	1	POL_HV1JR P20875 human immun
5	53	46.9	1015	1	POL_HV1B1 P03366 human immun
6	53	46.9	1015	1	POL_HV1B5 P04587 human immun
7	53	46.9	1015	1	POL_HV1BR P03367 human immun
8	53	46.9	1015	1	POL_HV1PV P03368 human immun
9	50	44.2	413	1	YIHS_ECOLI P32140 escherichia
10	48.5	42.9	859	1	ENV_EIAV3 P22429 equine infe
11	48	42.5	455	1	UHPT_CHLPN Q9z7n9 chlamydia p
12	48	42.5	456	1	UHPT_CHLMU Q9pjj8 chlamydia m
13	48	42.5	456	1	UHPT_CHLTR O84548 chlamydia t
14	48	42.5	1002	1	POL_HV1EL P04589 human immun
15	48	42.5	1002	1	POL_HV1MA P04588 human immun
16	48	42.5	1002	1	POL_HV1RH P05959 human immun
17	48	42.5	1002	1	POL_HV1Z2 P12499 human immun

18 48 42.5 1003 1 POL_HV1N5 P12497 human immun
19 48 42.5 1003 1 POL_HV1OY P20892 human immun
20 47 41.6 229 1 CEMA_SOYBN P49160 glycine max
21 47 41.6 633 1 GYP3_YEAST P48566 saccharomyc
22 47 41.6 1002 1 POL_HV1ND P18802 human immun
23 46 40.7 78 1 YO09_BPL2 P42544 bacterioph
24 46 40.7 229 1 CEMA_SPIOL Q9m314 spinacia ol
25 46 40.7 1103 1 CHS6_USTMA O13395 ustilago ma
26 46 40.7 1171 1 ZBE4_HUMAN O75132 homo sapien
27 45 39.8 238 1 YC53_PORPU P51202 porphyra pu
28 44.5 39.4 119 1 YF56_PYRFU Q8u0n0 pyrococcus
29 44.5 39.4 121 1 YF39_PYRHO O74017 pyrococcus
30 44.5 39.4 859 1 ENV_EIAV1 P22427 equine infe
31 44.5 39.4 859 1 ENV_EIAV2 P22428 equine infe
32 44.5 39.4 859 1 ENV_EIAV9 P11306 equine infe
33 44.5 39.4 859 1 ENV_EIACV P32541 equine infe
34 44.5 39.4 859 1 ENV_EIAVW P16082 equine infe
35 44.5 39.4 859 1 ENV_EIAVY P06751 equine infe
36 44.5 39.4 860 1 ENV_EIAV5 P22430 equine infe
37 44 38.9 280 1 RIP1_HORVU P22244 hordeum vul
38 44 38.9 280 1 RIP2_HORVU P04399 hordeum vul
39 44 38.9 612 1 OCTC_BOVIN O19094 bos taurus
40 44 38.9 1019 1 POL_SIVS4 P12502 simian immu
41 44 38.9 1022 1 POL_SIVSP P19505 simian immu
42 44 38.9 1054 1 POL_SIVMK P05897 simian immu
43 44 38.9 1056 1 POL_SIVM1 P05896 simian immu
44 43.5 38.5 472 1 E1BL_ADE41 P10546 human adeno
45 43 38.1 344 1 RHAT_ECOLI P27125 escherichia

Search completed: March 1, 2004, 19:25:00
Job time : 7.89623 secs

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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:40:39 ; Search time 31.8349 Seconds
(without alignments)
168.488 Million cell updates/sec

Title: US-09-915-914B-3
Perfect score: 113
Sequence: 1 YGFKRRQTWETWTE 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:**
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result Query			
No.	Score	Match Length DB ID	Description

1 56.5 50.0 524 15 Q9IDJ7 human immun
2 56.5 50.0 1009 15 Q8JAX3 human immun
3 55.5 49.1 524 15 Q9IDE9 human immun
4 55.5 49.1 524 15 Q9IDF8 human immun
5 55.5 49.1 560 15 Q9OS63 human immun
6 55.5 49.1 560 15 Q9OS45 human immun
7 55.5 49.1 560 15 Q9OS47 human immun
8 55.5 49.1 582 15 Q8Q898 human immun
9 55.5 49.1 588 15 Q8Q875 human immun
10 55.5 49.1 593 15 Q8Q887 human immun
11 55.5 49.1 1002 15 Q9IMZ9 human immun
12 55.5 49.1 1434 15 Q7SV29 human immun
13 53 46.9 212 15 Q9WGU7 human immun
14 53 46.9 225 15 Q998V3 human immun
15 53 46.9 237 15 Q9WGV0 human immun
16 53 46.9 237 15 Q9WGV3 human immun
17 53 46.9 237 15 Q9WGV7 human immun
18 53 46.9 237 15 Q9WGV5 human immun
19 53 46.9 237 15 Q9WGW0 human immun
20 53 46.9 237 15 Q9WGV5 human immun
21 53 46.9 237 15 Q9WGV9 human immun
22 53 46.9 237 15 Q9WBH5 human immun
23 53 46.9 237 15 Q9W9U0 human immun
24 53 46.9 237 15 Q9WGX6 human immun
25 53 46.9 237 15 Q9WGX7 human immun
26 53 46.9 237 15 Q9WGW2 human immun
27 53 46.9 237 15 Q9WGX5 human immun
28 53 46.9 237 15 Q9WGW1 human immun
29 53 46.9 237 15 Q9WGV2 human immun
30 53 46.9 237 15 Q9WGW8 human immun
31 53 46.9 237 15 Q9WGW6 human immun
32 53 46.9 237 15 Q9WGV6 human immun
33 53 46.9 237 15 Q9WGV8 human immun
34 53 46.9 237 15 Q9WGW3 human immun
35 53 46.9 237 15 Q9WGW4 human immun
36 53 46.9 237 15 Q9WGV1 human immun
37 53 46.9 237 15 Q9WGV4 human immun
38 53 46.9 433 15 Q79787 human immun
39 53 46.9 514 15 Q9DLJ8 human immun
40 53 46.9 519 15 Q9IDI3 human immun
41 53 46.9 523 15 Q9IDI9 human immun
42 53 46.9 523 15 Q9IDC7 human immun
43 53 46.9 523 15 Q9IDB6 human immun
44 53 46.9 523 15 Q9IDB2 human immun
45 53 46.9 523 15 Q9IDF2 human immune

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OM protein - protein search, using sw model

Run on: March 1, 2004, 13:31:13 ; Search time 50.3679 Seconds
(without alignments)
106.584 Million cell updates/sec

Title: US-09-915-914B-4
Perfect score: 132
Sequence: 1 YGFKKFERXPWTWETWTE 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB ID	Description
	Score	Match	Length		
1	132	100.0	19	5 ABB77668	Abb77668 Peptide t
2	132	100.0	19	5 ABB77698	Abb77698 Peptide t
3	132	100.0	19	5 ABB77669	Abb77669 Peptide t
4	122	92.4	20	5 ABB77679	Abb77679 Generic p
5	97.5	73.9	18	5 ABB77666	Abb77666 Peptide t
6	90	68.2	17	5 ABB77667	Abb77667 Peptide t
7	75	56.8	21	5 ABB77665	Abb77665 Peptide t
8	69	52.3	9	5 ABB77692	Abb77692 Peptide t
9	69	52.3	11	5 ABB77695	Abb77695 Peptide t

Search completed: March 1, 2004, 19:31:51
Job time : 32.8349 secs

07-FEB-2002.

26-JUL-2001; 2001WO-US023406.

31-JUL-2000; 2000US-0221932P.

(ACTI-) ACTIVE MOTIF.
(CNRS) CENT NAT RECH SCI.

Divida G, Morris M, Mery J, Heitz F, Fernandez J, Archdeacon J;
Horndorp K;

WPI; 2002-329441/36.

Transfection agent that comprises a peptide comprising hydrophobic and hydrophilic domain and having amino acid residues of specified length is useful for a non-covalent association with and transport of a heterologous compound into a cell.

Claim 12; Page 16; 156pp; English.

The invention relates to a transfection agent comprises a peptide of about 16 - 30 amino acids in length. Peptides of the invention comprise a hydrophobic domain, a hydrophilic domain, optionally a spacer sequence between the domains and a functional group conjugated to at least one terminal of the peptide. Peptides of the invention are useful for a non-covalent association with and transport of a heterologous compound into a cell. They are also useful for promoting the cellular internalisation of at least one member e.g. peptide, proteins, antibodies, their derivatives and/or conjugates. They may form part of a pharmaceutical composition to deliver the compound selected from a diagnostic or therapeutic compound, to treat at least one condition such as cancer or an infectious disease, or which targets a cancerous cell or pathogen-infected cell and to deliver a peptide or inhibitor that disrupts the activity of the enzyme. The agent of the invention has a transfection efficiency of at least 5% for at least two of the members of the group of the compounds. The agent has a good delivery efficiency for a broad spectrum of compounds and cell types, has a low toxicity, are easy to handle and easy to formulate in conjunction with the many different compound types that it can deliver. The peptides are serum sensitive, thus they bode particularly well for systemic and/or localised in patients. The current sequence represents the peptide transfection agent Pep-3

RESULT 1
ABB77668
ID ABB77668 standard; peptide; 19 AA.

Query Match 100.0%; Score 132; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.8e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 YGFKKFRKPWTWMTWTE 19
|||||

Dd

1 YGFKKFRKPWTWMTWTE 19

RESULT 2
ABB77698

PN WO200210201-A2.

ID XX ABB77698 standard; peptide; 19 AA.
XX AC ABB77698;
XX DT 01-JUL-2002 (first entry)
XX DE Peptide transfection agent Pep-4.1-Cya.
XX KW Intracellular delivery; transfection agent; cancer; infectious disease;
XX KW peptide vector.
XX OS Synthetic.
XX PN WO200210201-A2.
XX PD 07-FEB-2002.
XX PF 26-JUL-2001; 2001WO-US023406.
XX PR 31-JUL-2000; 2000US-0221932P.
XX PA (ACTI-) ACTIVE MOTIF.
XX PA (CNRS) CENT NAT RECH SCI.
XX PI Divida G, Morris M, Mery J, Heitz F, Fernandez J, Archdeacon J;
XX PI Horndorp K;
XX DR WPI; 2002-329441/36.
XX DR Transfection agent that comprises a peptide comprising hydrophobic and
PT hydrophilic domain and having amino acid residues of specified length is
PT useful for a non-covalent association with and transport of a
PT heterologous compound into a cell.
XX PS Example 4; Page 77; 156pp; English.
XX CC The invention relates to a transfection agent comprises a peptide of
CC about 16 - 30 amino acids in length. Peptides of the invention comprise a
CC hydrophobic domain, a hydrophilic domain, optionally a spacer sequence
CC between the domains and a functional group conjugated to at least one
CC terminal of the peptide. Peptides of the invention are useful for a non-
CC covalent association with and transport of a heterologous compound into a
CC cell. They are also useful for promoting the cellular internalisation of
CC at least one member e.g. peptide, proteins, antibodies, their derivatives
CC and/or conjugates. They may form part of a pharmaceutical composition to
CC deliver the compound selected from a diagnostic or therapeutic compound,
CC to treat at least one condition such as cancer or an infectious disease,
CC or which targets a cancerous cell or pathogen-infected cell and to
CC deliver a peptide or inhibitor that disrupts the activity of the enzyme.
CC The agent of the invention has a transfection efficiency of at least 5%
CC for at least two of the members of the group of the compounds. The agent
CC has a good delivery efficiency for a broad spectrum of compounds and cell
CC types, has a low toxicity, are easy to handle and easy to formulate in
CC conjunction with the many different compound types that it can deliver.
CC The peptides are serum sensitive, thus they bode particularly well for
CC systemic and/or localised in patients. The current sequence represents
CC the peptide transfection agent Pep-4.1-Cya

XX SQ Sequence 19 AA;
XX Query Match 100.0%; Score 132; DB 5; Length 19;
XX Best Local Similarity 100.0%; Pred.No. 5.8e-11;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 YGFKKFRKPWTWWTWTE 19
XX DB 1 YGFKKFRKPWTWWTWTE 19
XX RESULT 3
XX ABB77669
XX ID ABB77669 standard; peptide; 19 AA.
XX AC ABB77669;
XX DT 01-JUL-2002 (first entry)
XX DE Peptide transfection agent Pep-2.6.
XX KW Intracellular delivery; transfection agent; cancer; infectious disease;
XX KW peptide vector.
XX OS Synthetic.
XX PN WO200210201-A2.
XX PD 07-FEB-2002.
XX PF 26-JUL-2001; 2001WO-US023406.
XX PR 31-JUL-2000; 2000US-0221932P.
XX PA (ACTI-) ACTIVE MOTIF.
XX PA (CNRS) CENT NAT RECH SCI.
XX PI Divida G, Morris M, Mery J, Heitz F, Fernandez J, Archdeacon J;
XX PI Horndorp K;
XX DR WPI; 2002-329441/36.
XX PT Transfection agent that comprises a peptide comprising hydrophobic and
PT hydrophilic domain and having amino acid residues of specified length is
PT useful for a non-covalent association with and transport of a
PT heterologous compound into a cell.
XX PS Claim 12; Page 16; 156pp; English.
XX CC The invention relates to a transfection agent comprises a peptide of
CC about 16 - 30 amino acids in length. Peptides of the invention comprise a
CC hydrophobic domain, a hydrophilic domain, optionally a spacer sequence
CC between the domains and a functional group conjugated to at least one
CC terminal of the peptide. Peptides of the invention are useful for a non-
CC covalent association with and transport of a heterologous compound into a
CC cell. They are also useful for promoting the cellular internalisation of

CC at least one member e.g. peptide, proteins, antibodies, their derivatives
CC and/or conjugates. They may form part of a pharmaceutical composition to
CC deliver the compound selected from a diagnostic or therapeutic compound,
CC to treat at least one condition such as cancer or an infectious disease,
CC or which targets a cancerous cell or pathogen-infected cell and to
CC deliver a peptide or inhibitor that disrupts the activity of the enzyme.
CC The agent of the invention has a transfection efficiency of at least 5%
CC for at least two of the members of the group of the compounds. The agent
CC has a good delivery efficiency for a broad spectrum of compounds and cell
CC types, has a low toxicity, are easy to handle and easy to formulate in
CC conjunction with the many different compound types that it can deliver.
CC The peptides are serum sensitive, thus they bode particularly well for
CC systemic and/or localised in patients. The current sequence represents
CC the peptide transfection agent Pep-2.6
XX
SQ Sequence 19 AA;

Query Match 100.0%; Score 132; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.8e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGFKKFRKPWTWWETWTE 19
 |||||
Db 1 YGFKKFRKPWTWWETWTE 19

Search completed: March 1, 2004, 16:55:52
Job time : 62.3679 secs

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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:46:26 ; Search time 12.4575 Seconds
(without alignments)
146.709 Million cell updates/sec

Title: US-09-915-914B-4
Perfect score: 132
Sequence: 1 YGFKKFRKPWTWWETWTE 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %			DB ID	Description
		Match	Length			
1	54	40.9	332	2	E69312	nitrate reductase
2	54	40.9	1003	1	GNWLV	HIV-1 retropepsin
3	54	40.9	1003	1	B44001	HIV-1 retropepsin
4	54	40.9	1003	2	T09440	pol polyprotein -
5	54	40.9	1012	1	GNWVL	HIV-1 retropepsin
6	54	40.9	1015	1	GNWH3	HIV-1 retropepsin
7	53	40.2	392	2	G82746	hypothetical prote
8	53	40.2	559	2	B47175	reverse transcript
9	52	39.4	667	1	VCLJGL	env polyprotein pr
10	52	39.4	814	2	A95206	glycosyl transfera
11	52	39.4	902	2	T01668	pol polyprotein -
12	52	39.4	1002	2	S54378	pol polyprotein -
13	51.5	39.0	1780	2	A85045	probable glucan sy

14 50 37.9 130 2 A82599 conserved hypothet
15 49.5 37.5 148 2 S46515 puroindoline-a pre
16 49.5 37.5 222 2 A88102 protein W09G10.1 [
17 48.5 36.7 223 2 A29770 cerebellar degener
18 48.5 36.7 660 2 E81839 probable transmemb
19 48.5 36.7 675 2 E81101 transporter, BCO1
20 48.5 36.7 1103 2 T42022 probable chitin sy
21 48 36.4 1002 1 GNLJND HIV-1 retropepsin
22 47.5 36.0 625 2 T06184 sucrose-fructan 6-
23 47 35.6 86 2 T05982 hypothetical prote
24 47 35.6 198 2 G72489 hypothetical prote
25 47 35.6 227 2 AC0944 conserved hypothet
26 47 35.6 341 2 A83644 hypothetical prote
27 47 35.6 413 2 C91229 hypothetical prote
28 47 35.6 413 2 B86076 hypothetical prote
29 47 35.6 418 2 S40824 hypothetical 48K p
30 47 35.6 445 2 A41621 env polypeptide M
31 47 35.6 477 2 S52162 sucrose hydrolase
32 47 35.6 477 2 C91034 sucrose-6 phosphat
33 47 35.6 477 2 D85878 sucrose hydrolase
34 47 35.6 623 2 T47542 Spot 3 protein and
35 47 35.6 628 2 T02604 vacuolar sorting r
36 47 35.6 628 2 T02604 probable vacuolar
37 46.5 35.2 598 2 I51388 gamma-aminobutyric
38 46.5 35.2 794 2 S50687 hypothetical prote
39 46 34.8 221 2 F88082 protein T05A8.2 [i
40 46 34.8 262 2 F82519 hypothetical prote
41 46 34.8 469 2 T50934 dioxigenase Dita1,
42 46 34.8 624 2 T00044 vacuolar sorting r
43 46 34.8 625 2 F84706 probable vacuolar
44 46 34.8 643 2 AG0787 cytochrome c-type
45 46 34.8 643 2 AH0960 cytochrome c-type

Search completed: March 1, 2004, 19:34:28
Job time : 15.5485 secs

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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:39:39 ; Search time 7.70755 Seconds
(without alignments)
128.359 Million cell updates/sec

Title: US-09-915-914B-4
Perfect score: 132
Sequence: 1 YGFKKFKRPWTWETWTE 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	43.2	1006	1	POL_HV1MN P05961 human immun
2	55	41.7	789	1	LP1B_DROME P11996 drosophila
3	54	40.9	332	1	HMEC_ARCFU O29749 archaeoglob
4	54	40.9	1003	1	POL_HV1H2 P04585 human immun
5	54	40.9	1003	1	POL_HV1Y2 P35963 human immun
6	54	40.9	1007	1	POL_HV1JR P20875 human immun
7	54	40.9	1015	1	POL_HV1B1 P03366 human immun
8	54	40.9	1015	1	POL_HV1B5 P04587 human immun
9	54	40.9	1015	1	POL_HV1BR P03367 human immun
10	54	40.9	1015	1	POL_HV1PV P03368 human immun
11	52	39.4	667	1	ENV_GALV P21415 gibbon ape
12	52	39.4	1002	1	POL_HV1EL P04589 human immun
13	52	39.4	1002	1	POL_HV1MA P04588 human immun
14	52	39.4	1002	1	POL_HV1Z2 P12499 human immun
15	50	37.9	789	1	LP1A_DROME P11995 drosophila
16	49.5	37.5	148	1	PUIA_WHEAT P33432 triticum ae
17	49	37.1	856	1	ENV_HV2NZ P05883 human immun

18 49 37.1 1002 1 POL_HV1RH P05959 human immun
19 49 37.1 1003 1 POL_HV1N5 P12497 human immun
20 49 37.1 1003 1 POL_HV1OY P20892 human immun
21 48.5 36.7 223 1 CDR1_HUMAN P51861 homo sapien
22 48.5 36.7 1103 1 CHS6_USTMA O13395 ustilago ma
23 48 36.4 627 1 TES1_MOUSE C070146 mus musculu
24 48 36.4 1002 1 POL_HV1ND P18802 human immun
25 47 35.6 227 1 YIIY_SALFY P43022 salmonella
26 47 35.6 294 1 239F_HUMAN Q15777 homo sapien
27 47 35.6 413 1 YIHS_ECOLI P32140 escherichia
28 47 35.6 477 1 CSCA_ECOLI P40714 escherichia
29 46.5 35.2 794 1 YE14_YEAST P39961 saccharomyc
30 46 34.8 78 1 YO09_BPL2 P42544 bacterioph
31 46 34.8 330 1 CATK_PIG Q9gle3 sus scrofa
32 46 34.8 859 1 ENV_HV2CA P24105 human immun
33 46 34.8 859 1 ENV_HV2D2 P15831 human immun
34 46 34.8 1002 1 POL_HV1U4 P24740 human immun
35 46 34.8 1027 1 POL_SIVCZ P17283 chimpanzee
36 45.5 34.5 691 1 COMA_NEIGO P51973 neisseria g
37 45 34.1 132 1 YXEC_BACSU P54942 bacillus su
38 45 34.1 203 1 Y028_MYCPN P75083 mycoplasma
39 45 34.1 228 1 IFE2_CAEEL Q21693 caenorhabdi
40 45 34.1 329 1 CATK_RABIT P43236 oryctolagus
41 45 34.1 344 1 RHAT_ECOLI P27125 escherichia
42 45 34.1 372 1 SUM1_MOUSE Q8r0f3 mus musculu
43 45 34.1 374 1 SUM1_HUMAN Q8nbk3 homo sapien
44 45 34.1 377 1 CCHL_SCHPO O74794 schizosacch
45 45 34.1 393 1 DOM3_CAEEL Q10660 caenorhabdi

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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:40:39 ; Search time 35.5802 Seconds
(Without alignments)
168.488 Million cell updates/sec

Title: US-09-915-914B-4
Perfect score: 132
Sequence: 1 YGFKKFKRPWTWWTWTE 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archheap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query				
No.	Score	Match	Length	DB	ID

Description					

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
OM protein - protein search, using sw model
Run on: March 1, 2004, 13:31:13 ; Search time 50.3679 Seconds
(without alignments)
106.584 Million cell updates/sec

Title: US-09-915-914B-5
Perfect score: 132
Sequence: 1 YGFKKFRKPWTWWTWTE 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query				Description
	Score	Match	Length	ID	
1	132	100.0	19	5	ABB77668 Peptide t
2	132	100.0	19	5	ABB77698 Peptide t
3	132	100.0	19	5	ABB77669 Peptide t
4	122	92.4	20	5	ABB77679 Generic p
5	97.5	73.9	18	5	ABB77666 Peptide t
6	90	68.2	17	5	ABB77667 Peptide t
7	75	56.8	21	5	ABB77665 Peptide t
8	69	52.3	9	5	ABB77692 Peptide t
9	69	52.3	11	5	ABB77695 Peptide t

1	60	45.5	560	15	Q90RR5	Q90rr5 human immun
2	60	45.5	560	15	Q90RR6	Q90rr6 human immun
3	60	45.5	560	15	Q90RR4	Q90rr4 human immun
4	58	43.9	1033	15	Q79666	Q79666 human immun
5	57	43.2	225	15	Q998V3	Q998v3 human immun
6	57	43.2	237	15	Q9WGV3	Q9wgv3 human immun
7	57	43.2	237	15	Q9WGV7	Q9wgv7 human immun
8	57	43.2	237	15	Q9WGW5	Q9wgw5 human immun
9	57	43.2	237	15	Q9WGW0	Q9wgw0 human immun
10	57	43.2	237	15	Q9WGV5	Q9wgv5 human immun
11	57	43.2	237	15	Q9WGV9	Q9wgv9 human immun
12	57	43.2	237	15	Q9W8H5	Q9w8h5 human immun
13	57	43.2	237	15	Q9WGX6	Q9wgx6 human immun
14	57	43.2	237	15	Q9WGW2	Q9wgw2 human immun
15	57	43.2	237	15	Q9WGX5	Q9wgx5 human immun
16	57	43.2	237	15	Q9WGW6	Q9wgw6 human immun
17	57	43.2	237	15	Q9WGV6	Q9wgv6 human immun
18	57	43.2	237	15	Q9WGV8	Q9wgv8 human immun
19	57	43.2	237	15	Q9WGW3	Q9wgw3 human immun
20	57	43.2	237	15	Q9WGW4	Q9wgw4 human immun
21	57	43.2	237	15	Q9WGV4	Q9wgv4 human immun
22	57	43.2	519	15	Q9IDI3	Q9idi3 human immun
23	57	43.2	523	15	Q9IDI9	Q9idi9 human immun
24	57	43.2	523	15	Q9IDC7	Q9idc7 human immun
25	57	43.2	523	15	Q9IDF2	Q9idf2 human immun
26	57	43.2	524	15	Q9IDI8	Q9idi8 human immun
27	57	43.2	524	15	Q9IDI7	Q9idi7 human immun
28	57	43.2	524	15	Q9IDE9	Q9ide9 human immun
29	57	43.2	524	15	Q9IDD1	Q9idd1 human immun
30	57	43.2	524	15	Q9IDI6	Q9idi6 human immun
31	57	43.2	524	15	Q9IDF8	Q9idf8 human immun
32	57	43.2	524	15	Q9IDI2	Q9idi2 human immun
33	57	43.2	524	15	Q9IDI4	Q9idi4 human immun
34	57	43.2	524	15	Q9IDI5	Q9idi5 human immun
35	57	43.2	524	15	Q9IDD2	Q9idd2 human immun
36	57	43.2	547	15	Q90S79	Q90s79 human immun
37	57	43.2	547	15	Q90S76	Q90s76 human immun
38	57	43.2	547	15	Q90S80	Q90s80 human immun
39	57	43.2	547	15	Q90S77	Q90s77 human immun
40	57	43.2	547	15	Q90S81	Q90s81 human immun
41	57	43.2	547	15	Q90S78	Q90s78 human immun
42	57	43.2	560	15	Q90RS2	Q90rs2 human immun
43	57	43.2	560	15	Q90RP0	Q90rp0 human immun
44	57	43.2	560	15	Q99BA6	Q99ba6 human immun
45	57	43.2	560	15	Q71157	Q71157 human immun

Search completed: March 1, 2004, 19:31:52
Job time : 36.5802 secs

XX 07-FEB-2002.
XX
XX 26-JUL-2001; 2001WO-US023406.
XX
XX 31-JUL-2000; 2000US-0221932P.
PR
XX (ACTI-) ACTIVE MOTIF.
XX (CNRS) CENT NAT RECH SCI.
PA
XX Divida G, Morris M, Mery J, Heitz F, Fernandez J, Archdeacon J;
PI Horndorp K;
XX WPI; 2002-329441/36.
DR
XX Transfection agent that comprises a peptide comprising hydrophobic and
PT hydrophilic domain and having amino acid residues of specified length is
PT useful for a non-covalent association with and transport of a
PT heterologous compound into a cell.
XX
XX Claim 12; Page 16; 156pp; English.
XX
XX The invention relates to a transfection agent comprises a peptide of
CC about 16 - 30 amino acids in length. Peptides of the invention comprise a
CC hydrophobic domain, a hydrophilic domain, optionally a spacer sequence
CC between the domains and a functional group conjugated to at least one
CC terminal of the peptide. Peptides of the invention are useful for a non-
CC covalent association with and transport of a heterologous compound into a
CC cell. They are also useful for promoting the cellular internalisation of
CC at least one member e.g. peptide, proteins, antibodies, their derivatives
CC and/or conjugates. They may form part of a pharmaceutical composition to
CC deliver the compound selected from a diagnostic or therapeutic compound,
CC to treat at least one condition such as cancer or an infectious disease,
CC or which targets a cancerous cell or pathogen-infected cell and to
CC deliver a peptide or inhibitor that disrupts the activity of the enzyme.
CC The agent of the invention has a transfection efficiency of at least 5%

RESULT 1
ABE77668
ID ABE77668 standard; peptide; 19 AA.

DE Peptide transfection agent Pep-3.

D_b 1 YGKKFKPWTWWETWWT E 19

RESULT 2
ABB77698

PN WO200210201-A2.

ID ABB77698 standard; peptide; 19 AA.
 XX
 AC ABB77698;
 XX
 DT 01-JUL-2002 (first entry)
 XX
 DE Peptide transfection agent Pep-4.1-Cya.
 XX
 KW Intracellular delivery; transfection agent; cancer; infectious disease;
 peptide vector.
 XX
 OS Synthetic.
 XX
 PN WO200210201-A2.
 XX
 PD 07-FEB-2002.
 XX
 PF 26-JUL-2001; 2001WO-US023406.
 XX
 PR 31-JUL-2000; 2000US-0221932P.
 XX
 PA (ACTI-) ACTIVE MOTIF.
 (CNRS) CENT NAT RECH SCI.
 XX
 PI Divida G, Morris M, Mery J, Heitz F, Fernandez J, Archdeacon J;
 PI Horndorp K;
 XX
 DR WPI; 2002-329441/36.
 XX
 PT Transfection agent that comprises a peptide comprising hydrophobic and
 hydrophilic domain and having amino acid residues of specified length is
 useful for a non-covalent association with and transport of a
 heterologous compound into a cell.
 XX
 PS Example 4; Page 77; 156pp; English.
 XX
 CC The invention relates to a transfection agent comprises a peptide of
 about 16 - 30 amino acids in length. Peptides of the invention comprise a
 hydrophobic domain, a hydrophilic domain, optionally a spacer sequence
 between the domains and a functional group conjugated to at least one
 terminal of the peptide. Peptides of the invention are useful for a non-
 covalent association with and transport of a heterologous compound into a
 cell. They are also useful for promoting the cellular internalisation of
 at least one member e.g. peptide, proteins, antibodies, their derivatives
 and/or conjugates. They may form part of a pharmaceutical composition to
 deliver the compound selected from a diagnostic or therapeutic compound,
 to treat at least one condition such as cancer or an infectious disease,
 or which targets a cancerous cell or pathogen-infected cell and to
 deliver a peptide or inhibitor that disrupts the activity of the enzyme.
 The agent of the invention has a transfection efficiency of at least 5%
 for at least two of the members of the group of the compounds. The agent
 has a good delivery efficiency for a broad spectrum of compounds and cell
 types, has a low toxicity, are easy to handle and easy to formulate in
 conjunction with the many different compound types that it can deliver.
 The peptides are serum sensitive, thus they bode particularly well for
 systemic and/or localised in patients. The current sequence represents
 the peptide transfection agent Pep-4.1-Cya

CC at least one member e.g. peptide, proteins, antibodies, their derivatives
CC and/or conjugates. They may form part of a pharmaceutical composition to
CC deliver the compound selected from a diagnostic or therapeutic compound,
CC to treat at least one condition such as cancer or an infectious disease,
CC or which targets a cancerous cell or pathogen-infected cell and to
CC deliver a peptide or inhibitor that disrupts the activity of the enzyme.
CC The agent of the invention has a transfection efficiency of at least 5%
CC for at least two of the members of the group of the compounds. The agent
CC has a good delivery efficiency for a broad spectrum of compounds and cell
CC types, has a low toxicity, are easy to handle and easy to formulate in
CC conjunction with the many different compound types that it can deliver.
CC The peptides are serum sensitive, thus they bode particularly well for
CC systemic and/or localised in patients. The current sequence represents
CC the peptide transfection agent Pep-2.6
XX
SQ Sequence 19 AA;

Query Match 100.0%; Score 132; DE 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.8e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGFKKFRKPWTWWTWTE 19
| | | | | | | | | | | | | | | | | |
Db 1 YGFKKFRKPWTWWTWTE 19

Search completed: March 1, 2004, 16:55:52
Job time : 50.3679 secs

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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:46:26 ; Search time 12.4575 Seconds
(without alignments)
146.709 Million cell updates/sec

Title: US-09-915-914B-5
Perfect score: 132
Sequence: 1 YGFKKFRKPWTWWTWTE 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			DB ID	Description
		Match	Length	%		
1	54	40.9	332	2	E69312	nitrate reductase
2	54	40.9	1003	1	GNVWL	HIV-1 retropepsin
3	54	40.9	1003	1	B44001	HIV-1 retropepsin
4	54	40.9	1003	2	T09440	pol polyprotein -
5	54	40.9	1012	1	GNVWL	HIV-1 retropepsin
6	54	40.9	1015	1	GNVWH3	HIV-1 retropepsin
7	53	40.2	392	2	G82746	hypothetical prote
8	53	40.2	559	2	B47175	reverse transcript
9	52	39.4	667	1	VCLJGL	env polyprotein pr
10	52	39.4	814	2	A95206	glycosyl transfera
11	52	39.4	902	2	T01668	pol polyprotein -
12	52	39.4	1002	2	S54378	pol polyprotein -
13	51.5	39.0	1780	2	A85045	probable glucan sy

14 50 37.9 130 2 A82599 conserved hypothet
15 49.5 37.5 148 2 S46515 puroindoline-a pre
16 49.5 37.5 222 2 A88102 protein W09G10.1 [l
17 48.5 36.7 223 2 A29770 cerebellar degener
18 48.5 36.7 660 2 E81839 probable transmemb
19 48.5 36.7 675 2 E81101 transporter, B0CT
20 48.5 36.7 1103 2 T42022 probable chitin sy
21 48 36.4 1002 1 GNLJND HIV-1 retropepsin
22 47.5 36.0 625 2 T06184 sucrose-fructan 6-
23 47 35.6 86 2 T05982 hypothetical prote
24 47 35.6 198 2 G72489 hypothetical prote
25 47 35.6 227 2 AC0944 conserved hypothet
26 47 35.6 341 2 A83644 hypothetical prote
27 47 35.6 413 2 C91229 hypothetical prote
28 47 35.6 413 2 B86076 hypothetical prote
29 47 35.6 418 2 S40824 hypothetical 48K p
30 47 35.6 445 2 A41621 env polypoteins M
31 47 35.6 477 2 S52162 sucrose hydrolase
32 47 35.6 477 2 C91034 sucrose-6 phosphat
33 47 35.6 477 2 D85878 sucrose hydrolase
34 47 35.6 623 2 T47542 Spot 3 protein and
35 47 35.6 628 2 T02602 vacuolar sorting r
36 47 35.6 628 2 T02604 probable vacuolar
37 46.5 35.2 598 2 I51368 gamma-aminobutyric
38 46.5 35.2 794 2 S50687 hypothetical prote
39 46 34.8 221 2 F88082 protein T05A8.2 [i
40 46 34.8 262 2 F82519 hypothetical prote
41 46 34.8 469 2 T50934 dioxigenase Dita1,
42 46 34.8 624 2 T00044 vacuolar sorting r
43 46 34.8 625 2 F84706 probable vacuolar
44 46 34.8 643 2 AG0787 cytochrome c-type
45 46 34.8 643 2 AH0960 cytochrome c-type

Search completed: March 1, 2004, 19:34:28
Job time : 12.5485 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:46:26 ; Search time 12.4575 Seconds
(without alignments)
146.709 Million cell updates/sec

Title: US-09-915-914B-5
Perfect score: 132
Sequence: 1 YGFKKFRKPWTWWTWTE 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: Pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	54	40.9	332	2	E69312	nitrate reductase
2	54	40.9	1003	1	GNWLV	HIV-1 retropepsin
3	54	40.9	1003	1	B44001	HIV-1 retropepsin
4	54	40.9	1003	2	T09440	pol polypoteins -
5	54	40.9	1012	1	GNWVL	HIV-1 retropepsin
6	54	40.9	1015	1	GNWH3	HIV-1 retropepsin
7	53	40.2	392	2	G82746	hypothetical prote
8	53	40.2	559	2	B47175	reverse transcript
9	52	39.4	667	1	VCLJGL	env polypoteins pr
10	52	39.4	814	2	A95206	glycosyl transfera
11	52	39.4	902	2	T01668	pol polypoteins -
12	52	39.4	1002	2	S54378	pol polypoteins -
13	51.5	39.0	1780	2	A85045	probable glucan sy

14 50 37.9 130 2 A82599 conserved hypothet
15 49.5 37.5 148 2 S46515 puroindoline-a pre
16 49.5 37.5 222 2 A88102 protein W09G10.1 [
17 48.5 36.7 223 2 A29770 cerebellar degener
18 48.5 36.7 660 2 E81839 probable transmemb
19 48.5 36.7 675 2 E81101 transporter, BOC1
20 48.5 36.7 1103 2 T42022 probable chitin sy
21 48 36.4 1002 1 GNLJND HIV-1 retropepsin
22 47.5 36.0 625 2 T06184 sucrose-fructan 6-
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24 47 35.6 198 2 G72489 hypothetical prote
25 47 35.6 227 2 AC0944 conserved hypothet
26 47 35.6 341 2 A83644 hypothetical prote
27 47 35.6 413 2 C91229 hypothetical prote
28 47 35.6 413 2 B86076 hypothetical prote
29 47 35.6 418 2 S40824 hypothetical 48K p
30 47 35.6 445 2 A41621 env polypeptin M
31 47 35.6 477 2 S52162 sucrose hydrolase
32 47 35.6 477 2 C91034 sucrose-6 phosphat
33 47 35.6 477 2 D85878 sucrose hydrolase
34 47 35.6 623 2 T47542 Spot 3 protein and
35 47 35.6 628 2 T02602 vacuolar sorting r
36 47 35.6 628 2 T02604 probable vacuolar
37 46.5 35.2 598 2 I51368 gamma-aminobutyric
38 46.5 35.2 794 2 S50687 hypothetical prote
39 46 34.8 221 2 F88082 protein T05A8.2 [i
40 46 34.8 262 2 F82519 hypothetical prote
41 46 34.8 469 2 T50934 dioxxygenase Dita1,
42 46 34.8 624 2 T00044 vacuolar sorting r
43 46 34.8 625 2 F84706 probable vacuolar
44 46 34.8 643 2 AG0787 cytochrome c-type
45 46 34.8 643 2 AH0960 cytochrome c-type

Search completed: March 1, 2004, 19:34:28
Job time : 12.5485 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:39:39 ; Search time 7.70755 Seconds
(without alignments)
128.359 Million cell updates/sec

Title: US-09-915-914B-5
Perfect score: 132
Sequence: 1 YGFKKFKRPWTWETWTE 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	43.2	1006	1 POL_HV1MN	P05961 human immun
2	55	41.7	789	1 LP1B_DROME	P11996 drosophila
3	54	40.9	332	1 HMEC_ARCFU	O29749 archaeoglob
4	54	40.9	1003	1 POL_HV1H2	P04585 human immun
5	54	40.9	1003	1 POL_HV1Y2	P35963 human immun
6	54	40.9	1007	1 POL_HV1JR	P20875 human immun
7	54	40.9	1015	1 POL_HV1B1	P03366 human immun
8	54	40.9	1015	1 POL_HV1B5	P04587 human immun
9	54	40.9	1015	1 POL_HV1BR	P03367 human immun
10	54	40.9	1015	1 POL_HV1PV	P03368 human immun
11	52	39.4	667	1 ENV_GALV	P21415 gibbon ape
12	52	39.4	1002	1 POL_HV1EL	P04589 human immun
13	52	39.4	1002	1 POL_HV1MA	P04588 human immun
14	52	39.4	1002	1 POL_HV1Z2	P12499 human immun
15	50	37.9	789	1 LP1A_DROME	P11995 drosophila
16	49.5	37.5	148	1 PUIA_WHEAT	P33432 triticum ae
17	49	37.1	856	1 ENV_HV2NZ	P05883 human immun

18 49 37.1 1002 1 POL_HV1RH P05959 human immun
19 49 37.1 1003 1 POL_HV1N5 P12497 human immun
20 49 37.1 1003 1 POL_HV1OY P20892 human immun
21 48.5 36.7 223 1 CDRI_HUMAN P51861 homo sapien
22 48.5 36.7 1103 1 CHS6_USTMA O13395 ustilago ma
23 48 36.4 627 1 TES1_MOUSE O70146 mus musculu
24 48 36.4 1002 1 POL_HV1ND P18802 human immun
25 47 35.6 227 1 YIIY_SALTY P43022 salmonella
26 47 35.6 294 1 239F_HUMAN Q15777 homo sapien
27 47 35.6 413 1 YIHS_ECOLI P32140 escherichia
28 47 35.6 477 1 CSCA_ECOLI P40714 escherichia
29 46.5 35.2 794 1 YE14_YEAST P39961 saccharomyc
30 46 34.8 78 1 YO09_BPL2 P42544 bacterioph
31 46 34.8 330 1 CATK_PIG Q9gle3 sus scrofa
32 46 34.8 859 1 ENV_HV2CA P24105 human immun
33 46 34.8 859 1 ENV_HV2D2 P15831 human immun
34 46 34.8 1002 1 POL_HV1U4 P24740 human immun
35 46 34.8 1027 1 POL_SIVCZ P17283 chimpanzee
36 45.5 34.5 691 1 COMA_NEIGO P51973 neisseria g
37 45 34.1 132 1 YXEC_BACSU P54942 bacillus su
38 45 34.1 203 1 Y028_MYCPN P75083 mycoplasma
39 45 34.1 228 1 IFE2_CAEEL Q21693 caenorhabdi
40 45 34.1 329 1 CATK_RABIT P43236 oryctolagus
41 45 34.1 344 1 RHAT_ECOLI P27125 escherichia
42 45 34.1 372 1 SUMI_MOUSE Q8r0f3 mus musculu
43 45 34.1 374 1 SUMI_HUMAN Q8nbk3 homo sapien
44 45 34.1 377 1 CCHL_SCHPO O74794 schizosacch
45 45 34.1 393 1 DOM3_CAEEL Q10660 caenorhabdi

Search completed: March 1, 2004, 19:25:02
Job time : 8.70755 secs

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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:40:39 ; Search time 35.5802 Seconds
(without alignments)
168.488 Million cell updates/sec

Title: US-09-915-914B-5
Perfect score: 132
Sequence: 1 YGFKKFRKPWTWETWTE 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archheap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

§			
Result	Query		
No.	Score	Match Length	ID Description

1 60 45.5 560 15 Q90RR5
2 60 45.5 560 15 Q90RR6
3 60 45.5 560 15 Q90RR4
4 58 43.9 1033 15 Q79666
5 57 43.2 225 15 Q998V3
6 57 43.2 237 15 Q9GWV3
7 57 43.2 237 15 Q9GWV7
8 57 43.2 237 15 Q9GW5
9 57 43.2 237 15 Q9GW0
10 57 43.2 237 15 Q9GWV5
11 57 43.2 237 15 Q9GWV9
12 57 43.2 237 15 Q9W8H5
13 57 43.2 237 15 Q9WGX6
14 57 43.2 237 15 Q9WGW2
15 57 43.2 237 15 Q9WGX5
16 57 43.2 237 15 Q9WGW6
17 57 43.2 237 15 Q9WGV6
18 57 43.2 237 15 Q9WGV8
19 57 43.2 237 15 Q9WGW3
20 57 43.2 237 15 Q9WGW4
21 57 43.2 237 15 Q9WGV4
22 57 43.2 519 15 Q9IDI3
23 57 43.2 523 15 Q9IDI9
24 57 43.2 523 15 Q9IDC7
25 57 43.2 523 15 Q9IDF2
26 57 43.2 524 15 Q9IDI8
27 57 43.2 524 15 Q9IDI7
28 57 43.2 524 15 Q9IDE9
29 57 43.2 524 15 Q9IDD1
30 57 43.2 524 15 Q9IDI6
31 57 43.2 524 15 Q9IDF8
32 57 43.2 524 15 Q9IDI2
33 57 43.2 524 15 Q9IDI4
34 57 43.2 524 15 Q9IDI5
35 57 43.2 524 15 Q9IDD2
36 57 43.2 547 15 Q9OS79
37 57 43.2 547 15 Q9OS76
38 57 43.2 547 15 Q9OS80
39 57 43.2 547 15 Q9OS77
40 57 43.2 547 15 Q9OS81
41 57 43.2 547 15 Q9OS78
42 57 43.2 560 15 Q9ORS2
43 57 43.2 560 15 Q9ORP0
44 57 43.2 560 15 Q99BA6
45 57 43.2 560 15 Q71157

Search completed: March 1, 2004, 19:31:52
Job time : 35.5802 secs

Q90rr5 human immun
Q90rr6 human immun
Q90rr4 human immun
Q79666 human immun
Q998v3 human immun
Q9wgv3 human immun
Q9wgv7 human immun
Q9wgv5 human immun
Q9wgv0 human immun
Q9wgv5 human immun
Q9w8h5 human immun
Q9wgv6 human immun
Q9wgv2 human immun
Q9wgv5 human immun
Q9wgv6 human immun
Q9wgv8 human immun
Q9wgv3 human immun
Q9wgv4 human immun
Q9wgv4 human immun
Q9idi3 human immun
Q9idi9 human immun
Q9idc7 human immun
Q9idf2 human immun
Q9idi8 human immun
Q9idi7 human immun
Q9ide9 human immun
Q9idd1 human immun
Q9idi6 human immun
Q9idf8 human immun
Q9idi2 human immun
Q9idi4 human immun
Q9idi5 human immun
Q9idd2 human immun
Q9os79 human immun
Q9os76 human immun
Q9os80 human immun
Q9os77 human immun
Q9os81 human immun
Q9os78 human immun
Q9ors2 human immun
Q9orpo human immun
Q99ba6 human immun
Q71157 human immun

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OM protein - protein search, using sw model

Run on: March 1, 2004, 13:31:13 ; Search time 50.3679 Seconds
(without alignments)
106.584 Million cell updates/sec

Title: US-09-915-914B-6
Perfect score: 119
Sequence: 1 KKKRKVKPETWETWETV 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 292547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query %			DB ID	Description
	Score	Match	Length		
1	119	100.0	19	5 ABB77670	Abb77670 Peptide t
2	74	62.2	20	5 ABB77694	Abb77694 Peptide t
3	74	62.2	21	5 ABB77674	Abb77674 Peptide t
4	70	58.8	19	5 ABB10106	Abb10106 Peptide t
5	70	58.8	19	5 ABB77699	Abb77699 Peptide t
6	69	58.0	19	5 ABB77668	Abb77668 Peptide t
7	69	58.0	19	5 ABB77698	Abb77698 Peptide t
8	69	58.0	19	5 ABB77669	Abb77669 Peptide t
9	68	57.1	20	5 ABB77679	Abb77679 Generic p

10 66.5 55.9 17 5 ABB77667 Abb77667 Peptide t
11 64.5 54.2 18 5 ABB77666 Abb77666 Peptide t
12 64 53.8 11 5 ABB77695 Abb77695 Peptide t
13 64 53.8 12 5 ABB77689 Abb77689 Hydrophob
14 64 53.8 12 5 ABP56174 Abp56174 Cell-targ
15 64 53.8 19 5 ABB77676 Abb77676 Peptide t
16 64 53.8 20 5 ABB77672 Abb77672 Peptide t
17 64 53.8 20 5 ABB77673 Abb77673 Peptide t
18 64 53.8 21 5 ABG78995 Abg78995 Cell pene
19 64 53.8 21 5 ABB77693 Abb77693 Peptide t
20 64 53.8 21 5 ABB77671 Abb77671 Peptide t
21 64 53.8 21 7 ADB68484 Adb68484 Peptide s
22 64 53.8 21 7 ADC22460 Adc22460 Protein-d
23 64 53.8 26 5 ABP56200 Abp56200 Chimeric
24 61 51.3 21 5 ABB77665 Abb77665 Peptide t
25 59 49.6 9 5 ABB77692 Abb77692 Peptide t
26 57 47.9 418 3 AAB35809 Aab35809 Mannose i
27 57 47.9 496 4 ABG25893 Abg25893 Novel hum
28 57 47.9 928 4 ABG30068 Abg30068 Novel hum
29 57 47.9 928 4 ABG29926 Abg29926 Novel hum
30 55 46.2 1510 5 ABB91970 Abb91970 Herbicida
31 55 46.2 1662 5 ABB93630 Abb93630 Herbicida
32 55 46.2 1858 5 ABB90859 Abb90859 Herbicida
33 54 45.4 21 5 ABB77678 Abb77678 Generic p
34 53.5 45.0 19 5 ABB77675 Abb77675 Peptide t
35 52 43.7 265 4 AAB80417 Aab80417 Gene #3 a
36 52 43.7 286 3 AAG54774 Aag54774 Arabidops
37 52 43.7 383 3 AAG42073 Aag42073 Arabidops
38 52 43.7 432 3 AAG42072 Aag42072 Arabidops
39 52 43.7 435 3 AAG42071 Aag42071 Arabidops
40 52 43.7 784 5 ABB92019 Abb92019 Herbicida
41 52 43.7 1346 3 AAG39112 Aag39112 Arabidops
42 52 43.7 1390 3 AAG39111 Aag39111 Arabidops
43 52 43.7 1403 3 AAG39110 Aag39110 Arabidops
44 51 42.9 24 4 AAM60395 Aam60395 Human bra
45 51 42.9 24 4 ABG54745 Abg54745 Human liv

ALIGNMENTS

RESULT 1
ABB77670
ID ABB77670 standard; peptide; 19 AA.

XX AC ABB77670;
XX DT 01-JUL-2002 (first entry)
XX DE Peptide transfection agent Pep-2.7.
XX KW Intracellular delivery; transfection agent; cancer; infectious disease;
XX KW peptide vector.
XX OS Synthetic.
XX PN W0200210201-A2.

XX 07-FEB-2002.
PD 26-JUL-2001; 2001WO-US023406.
XX PF 31-JUL-2000; 2000US-0221932P.
XX PR (ACTI-) ACTIVE MOTIF.
XX PA (CNRS) CENT NAT RECH SCI.
XX PI Divida G, Morris M, Mery J, Heitz F, Fernandez J, Archdeacon J;
PI Horndorp K;
XX WPI; 2002-329441/36.
XX Transfection agent that comprises a peptide comprising hydrophobic and
PT hydrophilic domain and having amino acid residues of specified length is
PT useful for a non-covalent association with and transport of a
PT heterologous compound into a cell.
XX Claim 12; Page 16; 156pp; English.
PS The invention relates to a transfection agent comprises a peptide of
XX about 16 - 30 amino acids in length. Peptides of the invention comprise a
CC hydrophobic domain, a hydrophilic domain, optionally a spacer sequence
CC between the domains and a functional group conjugated to at least one
CC terminal of the peptide. Peptides of the invention are useful for a non-
CC covalent association with and transport of a heterologous compound into a
CC cell. They are also useful for promoting the cellular internalisation of
CC and/or conjugates. They may form part of a pharmaceutical composition to
CC deliver the compound selected from a diagnostic or therapeutic compound,
CC to treat at least one condition such as cancer or an infectious disease,
CC or which targets a cancerous cell or pathogen-infected cell and to
CC deliver a peptide or inhibitor that disrupts the activity of the enzyme.
CC The agent of the invention has a transfection efficiency of at least 5%
CC for at least two of the members of the group of the compounds. The agent
CC has a good delivery efficiency for a broad spectrum of compounds and cell
CC types, has a low toxicity, are easy to handle and easy to formulate in
CC conjunction with the many different compound types that it can deliver.
CC The peptides are serum sensitive, thus they bode particularly well for
CC systemic and/or localised in patients. The current sequence represents
CC the peptide transfection agent Pep-2.7
XX
SQ Sequence 19 AA;

Query Match 100.0%; Score 119; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKKRKVKPETWETWETV 19
|
Db 1 KKKRKVKPETWETWETV 19

Search completed: March 1, 2004, 16:55:55
Job time : 53.3679 secs

OM protein - protein search, using sw model

Run on: March 1, 2004, 16:46:26 ; Search time 12.4575 Seconds
(without alignments)
146.709 Million cell updates/sec

Title: US-09-915-914B-6
Perfect score: 119
Sequence: 1 KKKRAVKPBTWETWETV 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.78: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB ID	Description
	Score	Match	Length		
1	57	47.9	418	2 S40824	hypothetical 48K p
2	55	46.2	352	2 G84352	general stress pro
3	55	46.2	1510	2 C84727	probable glucan sy
4	55	46.2	1878	2 E86189	hypothetical prote
5	54	45.4	413	2 C91229	hypothetical prote
6	54	45.4	413	2 B86076	hypothetical prote
7	52	43.7	784	2 E84785	probable glucan sy
8	51	42.9	390	1 A60424	calsequestrin prec
9	51	42.9	395	1 A25887	calsequestrin prec
10	51	42.9	1036	2 T05687	beta-galactosidase
11	50.5	42.4	571	2 C90391	hypothetical prote
12	49.5	41.6	1002	1 GNLJND	HIV-1 retropepsin
13	49.5	41.6	1003	1 GNVWL	HIV-1 retropepsin

14	49.5	41.6	1003	1 B44001	HIV-1 retropepsin
15	49.5	41.6	1003	2 T09440	pol polyprotein -
16	49.5	41.6	1012	1 GNVWL	HIV-1 retropepsin
17	49.5	41.6	1015	1 GNVWH3	HIV-1 retropepsin
18	49	41.2	683	2 T00872	probable protein x
19	48.5	40.8	766	2 S37894	hypothetical prote
20	48	40.3	197	2 S53053	hypothetical prote
21	48	40.3	314	2 T32293	hypothetical prote
22	48	40.3	797	2 JC4078	protective surface
23	48	40.3	808	2 F64102	hypothetical prote
24	47.5	39.9	463	2 T48116	reverse transcript
25	47.5	39.9	559	2 B47175	hypothetical prote
26	47	39.5	247	2 T37820	hypothetical prote
27	47	39.5	292	2 T30321	hypothetical prote
28	47	39.5	322	1 HLHUR2	T-cell surface gly
29	47	39.5	1963	2 T49914	cyclic beta 1-2 gl
30	47	39.5	2831	2 T31419	callose synthase c
31	47	39.5	2867	2 AG3481	cellobiose-phospho
32	46.5	39.1	1002	2 S54378	pol polyprotein -
33	46	38.7	119	2 D84845	hypothetical prote
34	46	38.7	331	2 A61046	ecdysone-induced m
35	46	38.7	510	2 D70480	acetyl-coenzyme A
36	46	38.7	513	2 E72495	probable acetyl-co
37	46	38.7	524	2 AB2338	acetyl-coenzyme A
38	46	38.7	558	2 G69126	acetyl-CoA synthet
39	46	38.7	645	2 A83054	acetyl-coenzyme A
40	46	38.7	646	2 C86441	probable ABC trans
41	46	38.7	647	2 C87693	acetyl-CoA synthet
42	46	38.7	647	2 E82579	acetyl coenzyme A
43	46	38.7	649	2 D75270	acetyl-CoA synthas
44	46	38.7	651	2 D70789	probable acetyl-co
45	46	38.7	651	2 D83534	acetyl-coenzyme A

Search completed: March 1, 2004, 19:34:30
Job time : 14.5485 secs

OM protein - protein search, using sw model

Run on: March 1, 2004, 16:39:39 ; Search time 7.70755 Seconds
(without alignments)
128.359 Million cell updates/sec

Title: US-09-915-914B-6
Perfect score: 119
Sequence: 1 KKRKVKPETWETWETV 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query				Description
	Score	Match	Length	ID	
1	57	47.9	413	1 YIHS_ECOLI	P32140 escherichia
2	51	42.9	390	1 CAQ1_HUMAN	P31415 homo sapien
3	51	42.9	395	1 CAQ1_RABIT	P07221 oryctolagus
4	51	42.9	399	1 CAQ1_MOUSE	O09165 mus musculu
5	49.5	41.6	504	1 YC03_KLEPN	Q48449 klebsiella
6	49.5	41.6	1002	1 POL_HV1ND	P18802 human immun
7	49.5	41.6	1003	1 POL_HV1H2	P04585 human immun
8	49.5	41.6	1003	1 POL_HV1Y2	P35963 human immun
9	49.5	41.6	1007	1 POL_HV1JR	P20875 human immun
10	49.5	41.6	1015	1 POL_HV1B1	P03366 human immun
11	49.5	41.6	1015	1 POL_HV1B5	P04587 human immun
12	49.5	41.6	1015	1 POL_HV1BR	P03367 human immun
13	49.5	41.6	1015	1 POL_HV1PV	P03368 human immun
14	48.5	40.8	766	1 STB6_YEAST	P36085 saccharomyc
15	48	40.3	793	1 D153_HAEIN	Q32629 haemophilus
16	48	40.3	795	1 D152_HAEIN	P44935 haemophilus
17	48	40.3	797	1 D151_HAEIN	P46024 haemophilus

18	47	39.5	51	1 Y04J_BPT4	P39490 bacteriopha
19	47	39.5	247	1 YE95_SCHPO	O13767 schizosacch
20	47	39.5	322	1 CD1E_HUMAN	P15812 homo sapien
21	46.5	39.1	1002	1 POL_HV1EL	P04589 human immun
22	46.5	39.1	1002	1 POL_HV1Z2	P12499 human immun
23	46.5	39.1	1006	1 POL_HV1MN	P05961 human immun
24	46	38.7	641	1 ACSA_PRB01	Q9f7r5 gamma-prote
25	46	38.7	644	1 ACS2_PSEPK	Q88dw6 pseudomonas
26	46	38.7	645	1 ACS2_PSEAE	Q9hv66 pseudomonas
27	46	38.7	647	1 ACSA_CAUCR	Q9a2i0 caulobacter
28	46	38.7	647	1 ACSA_XANAC	Q8pf09 xanthomonas
29	46	38.7	647	1 ACSA_XANCP	Q8p3i1 xanthomonas
30	46	38.7	647	1 ACSA_XYLFA	Q9pb89 xylella fas
31	46	38.7	647	1 ACSA_XYLFT	Q87c00 xylella fas
32	46	38.7	648	1 ACSA_BRAJA	Q89wv5 bradyrhizob
33	46	38.7	649	1 ACS2_RHIME	Q92kx2 rhizobium m
34	46	38.7	649	1 ACSA_DEIRA	Q9rrl7 deinococcus
35	46	38.7	649	1 ACSA_VIBCH	Q9kv59 vibrio chol
36	46	38.7	650	1 ACSA_SHEON	Q8edk3 shewanella
37	46	38.7	650	1 ACSA_VIBPA	Q87ku7 vibrio para
38	46	38.7	650	1 ACSA_VIBVU	Q8dcz9 vibrio vuln
39	46	38.7	651	1 ACS1_PSEAE	Q9i558 pseudomonas
40	46	38.7	651	1 ACSA_AGR5	Q8ubv5 agrobacteri
41	46	38.7	651	1 ACSA_BRUME	Q8vj48 brucella me
42	46	38.7	651	1 ACSA_BRUSU	Q8fyq3 brucella su
43	46	38.7	651	1 ACSA_MYCBO	P59871 mycobacteri
44	46	38.7	651	1 ACSA_MYCTU	O69635 mycobacteri
45	46	38.7	651	1 ACSA_PSESM	Q885k7 pseudomonas

Search completed: March 1, 2004, 19:25:02
Job time : 7.70755 secs

OM protein - protein search, using sw model

Run on: March 1, 2004, 16:40:39 ; Search time 35.5802 Seconds
(without alignments)
168.488 Million cell updates/sec

Title: US-09-915-914B-6
Perfect score: 119
Sequence: 1 KKRKRVKPETWETWETV 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL.25:*

1:	sp_archaea:*
2:	sp_bacteria:*
3:	sp_fungi:*
4:	sp_human:*
5:	sp_invertebrate:*
6:	sp_mammal:*
7:	sp_mhc:*
8:	sp_organelle:*
9:	sp_phage:*
10:	sp_plant:*
11:	sp_rodent:*
12:	sp_virus:*
13:	sp_vertebrate:*
14:	sp_unclassified:*
15:	sp_rvirus:*
16:	sp_bacteriap:*
17:	sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%			
Result	Query		
No.	Score	Match Length	ID Description

Q8tvul	methanopyru
Q7ub71	shigella fl
Q83iv0	shigella fl
Q88tu3	lactobacill
Q9hnn3	halobacteri
Q8gyw2	arabidopsis
Q9lr43	arabidopsis
Q7xjc6	oryza sativ
Q9ltg5	arabidopsis
Q9sl03	arabidopsis
Q9syj7	arabidopsis
Q9aue0	arabidopsis
Q9bpc0	conus tessu
Q8x8d6	escherichia
Q36164	actinophage
Q8ssu9	oryza sativ
Q89906	sugar beet
Q08534	sugar beet
Q9q703	sugar beet
Q9bpc5	conus ventr
Q9shn5	arabidopsis
Q82gv6	streptomyce
Q9sjm0	arabidopsis
Q8q879	human immun
Q8mia4	sus scrofa
Q9szn8	arabidopsis
Q8iak1	plasmodium
Q9idj7	human immun
Q97wk0	sulfolobus
Q8jax3	human immun
Q9bpc9	conus ventr
Q96lf2	drosophila
Q9vn28	drosophila
Q9lwu7	oryza sativ
Q8mvv0	plasmodium
Q9wgu7	human immun
Q9wgv0	human immun
Q9wgy5	human immun
Q9wgx9	human immun
Q9wgy7	human immun
Q9wgy3	human immun
Q9w9u0	human immun
Q9wgy1	human immun
Q9wgv2	human immun
Q9wgu8	human immun

Search completed: March 1, 2004, 19:31:58
Job time : 41.5802 secs